GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 21 Seconds
(without alignments)
41.225 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	67.7	577	2	B37057	integrin beta-6 ch
2	44	67.7	788	2	A37057	integrin beta-6 ch
3	43	66.2	1076	2	T26044	hypothetical prote
4	43	66.2	1627	2	S65464	pregnancy-associat
5	43	66.2	4753	1	A47437	LDL-receptor-relat
6	42.5	65.4	48	2	S29216	neurotoxin Tx2 - s
7	42.5	65.4	49	2	S29215	neurotoxin Tx2 - s
8	42.5	65.4	53	2	S29214	neurotoxin Tx2 - s
9	41	63.1	69	2	A55011	metallothionein-li
10	41	63.1	458	2	A84306	hypothetical prote
11	41	63.1	736	2	T06757	hypothetical prote
12	41	63.1	3672	2	T23433	hypothetical prote
13	41	63.1	3704	2	T37316	probable laminin a
14	40	61.5	195	1	TVVPA	small T antigen -
15	40	61.5	195	2	S22562	small T antigen -
16	40	61.5	313	2	S44208	extracellular matr
17	40	61.5	421	1	TVVPMP	middle T antigen -
18	40	61.5	421	2	S22561	middle T antigen -
19	40	61.5	440	1	TVVPM	middle T antigen -
20	39.5	60.8	246	2	A24609	acidic epididymal
21	39	60.0	30	2	JX0057	trypsin inhibitor
22	39	60.0	32	2	A05076	metallothionein -
23	39	60.0	50	2	T38209	probable metalloth
24	39	60.0	60	2	S30567	metallothionein -
25	39	60.0	60	2	JC2420	metallothionein -
26	39	60.0	61	1	SMBO2	metallothionein II
27	39	60.0	61	2	S00808	metallothionein Ia
28	39	60.0	61	2	S00810	metallothionein Ic
29	39	60.0	61	2	S00809	metallothionein Ib
30	39	60.0	61	2	I46602	metallothionein -
31	39	60.0	68	2	S44392	metallothionein 3
32	39	60.0	656	2	JC2005	integrin beta-5 ch
33	39	60.0	799	2	A38308	integrin beta-5 ch
34	39	60.0	850	2	S56015	gastric mucin MUC5
35	39	60.0	1182	2	I48378	hairless protein -
36	39	60.0	1291	2	T21694	hypothetical prote
37	39	60.0	1321	2	JE0352	mucin MUC5B, trach
38	39	60.0	1373	2	JE0095	gastric mucin MUC5
39	39	60.0	1513	2	A54895	mucin 2, intestina
40	39	60.0	3020	2	A43932	mucin 2 precursor,
41	38.5	59.2	788	2	I51530	integrin beta-3 su
42	38	58.5	40	1	SMFF	metallothionein Mt
43	38	58.5	40	2	B61194	metallothionein Mt
44	38	58.5	60	2	S31723	metallothionein -
45	38	58.5	60	2	B27490	metallothionein B

ALIGNMENTS

RESULT 1
B37057
integrin beta-6 chain - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 20-Aug-1999
C;Accession: B37057
R;Sheppard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.
J. Biol. Chem. 265, 11502-11507, 1990
A;Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identifie
A;Reference number: A37057; MUID:90307659; PMID:2365683
A;Accession: B37057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-577 <SHE>
A;Cross-references: GB:M35197; GB:J05522; NID:g191277; PIDN:AAA37043.1; PID:g553845
A;Note: the authors translated the codon AAA for residue 88 as Asn, AAC for residue 97 as
as Pro, ACG for residue 355 as Met, GAG for residue 363 as Thr, ACC for residue 364 as Al
Gly
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
C;Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match 67.7%; Score 44; DB 2; Length 577;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        370 CSGRGDCYC 378
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RESULT 2
A37057
integrin beta-6 chain - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 19-Jan-2001
C;Accession: A37057; I69201
R;Sheppard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.
J. Biol. Chem. 265, 11502-11507, 1990
A;Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identifie
A;Reference number: A37057; MUID:90307659; PMID:2365683
A;Accession: A37057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-788 <SHE>
A;Cross-references: GB:M35198; GB:J05522; NID:g186506; PIDN:AAA36122.1; PID:g186507
R;Jiang, W.M.; Jenkins, D.; Yuan, Q.; Leung, E.; Choo, K.H.; Watson, J.D.; Krissansen, G.
Int. Immunol. 4, 1031-1040, 1992
A;Title: The gene organization of the human beta 7 subunit, the common beta subunit of th
A;Reference number: I54749; MUID:93002753; PMID:1382574
A;Accession: I69201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 116-157,'R',159-197 <JIA>
A;Cross-references: GB:S49380; NID:g257588; PIDN:AAB23690.1; PID:g257589
C;Genetics:
A;Gene: GDB:ITGB6
A;Cross-references: GDB:131392; OMIM:147558
A;Map position: 2pter-2qter
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
C;Keywords: blocked amino end; cell adhesion; cytoskeleton; glycoprotein; lipoprotein; m
F;708-730/Domain: transmembrane #status predicted <TRM>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;7/Binding site: palmitate (Cys) (covalent) #status predicted
F;16,48,97,260,387,396,463,471/Binding site: carbohydrate (Asn) (covalent) #status predi

  Query Match 67.7%; Score 44; DB 2; Length 788;
  Best Local Similarity 66.7%; Pred. No. 35;
  Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 511 CSGRGDCYC 519

RESULT 3
T26044
hypothetical protein W01C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26044
R;Nhan, M.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid W01C8.
A;Reference number: Z20142
A;Accession: T26044
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1076 <NHA>
A;Cross-references: EMBL:U41508; PIDN:AAA82623.1; CESP:W01C8.3
C;Genetics:
A;Gene: CESP:W01C8.3
A;Introns: 59/3; 92/2; 157/3; 189/3; 220/2; 251/3; 275/2; 319/1; 374/3; 407/2

  Query Match 66.2%; Score 43; DB 2; Length 1076;
  Best Local Similarity 85.7%; Pred. No. 62;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDCRGDC 7
Db 276 CGCRGDC 282

RESULT 4
S65464
pregnancy-associated plasma protein A precursor - human
N;Alternate names: PAPP-A
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 05-Nov-1999
C;Accession: S65464; S65463; A54220; I38097
R;Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
submitted to the EMBL Data Library, June 1995
A;Description: Complete cDNA sequence of the preproform of human pregnancy-associated pl
A;Reference number: S65464
A;Accession: S65464
A;Molecule type: mRNA
A;Residues: 1-1627 <HAA>
A;Cross-references: EMBL:U28727; NID:g1142969; PIDN:AAC50543.1; PID:g1142970
R;Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Eur. J. Biochem. 237, 159-163, 1996
A;Title: Complete cDNA sequence of the preproform of human pregnancy-associated plasma p
A;Reference number: S65463; MUID:96203921; PMID:8620868
A;Accession: S65463
A;Molecule type: mRNA
A;Residues: 1-102 <HAW>
A;Cross-references: EMBL:U28727
A;Note: the authors translated the codon CGA for residue 101 as Thr
R;Kristensen, T.; Oxvig, C.; Sand, O.; Moller, N.P.H.; Sottrup-Jensen, L.
Biochemistry 33, 1592-1598, 1994
A;Title: Amino acid sequence of human pregnancy-associated plasma protein-A derived from
A;Reference number: A54220; MUID:94146014; PMID:7508748
A;Accession: A54220
A;Molecule type: mRNA
A;Residues: 77-1627 <KRI>
A;Cross-references: GB:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
R;Oxvig, C.; Sand, O.; Kristensen, T.; Gleich, G.J.; Sottrup-Jensen, L.
J. Biol. Chem. 268, 12243-12246, 1993
A;Title: Circulating human pregnancy-associated plasma protein-A is disulfide-bridged to
A;Reference number: I38097; MUID:93286045; PMID:7685339
A;Accession: I38097
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 77-1627 <RES>
A;Cross-references: EMBL:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
C;Genetics:
A;Gene: GDB:PAPPA
A;Cross-references: GDB:134729; OMIM:176385
A;Map position: 9q33.1-9q33.1
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-80/Domain: propeptide #status predicted <PRO>
F;81-1627/Product: pregnancy-associated plasma protein A #status predicted <MAT>

  Query Match 66.2%; Score 43; DB 2; Length 1627;
  Best Local Similarity 66.7%; Pred. No. 85;
  Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1600 CDLQGDCAC 1608

RESULT 5
A47437
LDL-receptor-related protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C;Accession: A47437; S27801; T21547
R;Yochem, J.; Greenwald, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 4572-4576, 1993
A;Title: A gene for a low density lipoprotein receptor-related protein in the nematode Ca
A;Reference number: A47437; MUID:93281621; PMID:8506301
A;Accession: A47437
A;Molecule type: DNA
A;Residues: 1-4753 <YOC>
A;Cross-references: GB:M96150; NID:g156359; PIDN:AAA28105.1; PID:g156360
A;Note: nucleotide sequence not given; translation not complete in this paper
R;Yochem, J.; Greenwald, I.
submitted to the EMBL Data Library, July 1992
A;Description: A gene for an LDL receptor-related protein (LPR) in the nematode C.elegans
A;Reference number: S27801
A;Accession: S27801
A;Molecule type: DNA
A;Residues: 1-4753 <YO2>
A;Cross-references: EMBL:M96150; NID:g156359; PIDN:AAA28105.1; PID:g156360
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19439
A;Accession: T21547
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4753 <WIL>
A;Cross-references: EMBL:Z73907; PIDN:CAA98124.1; GSPDB:GN00019; CESP:F29D11.1
A;Experimental source: clone F29D11
C;Genetics:
A;Gene: LPR
A;Map position: 1
A;Introns: 31/1; 88/1; 132/1; 172/3; 219/1; 298/1; 463/2; 526/2; 585/3; 780/2; 874/2; 975
15/1
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

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C;Keywords: tandem repeat; transmembrane protein
F;53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;92-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;223-257/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;302-336/Domain: EGF homology <EGF1>
F;1054-1095/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1101-1138/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;1146-1182/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;1187-1223/Domain: LDL receptor ligand-binding repeat homology <LD10>
F;1228-1263/Domain: LDL receptor ligand-binding repeat homology <LD11>
F;1270-1307/Domain: LDL receptor ligand-binding repeat homology <LD12>
F;1313-1350/Domain: LDL receptor ligand-binding repeat homology <LD13>
F;1359-1396/Domain: LDL receptor ligand-binding repeat homology <LD14>
F;1441-1475/Domain: EGF homology <EGF>
F;1611-1654/Domain: LDL receptor YWTD-containing repeat homology <YW33>
F;2792-2829/Domain: LDL receptor ligand-binding repeat homology <LD15>
F;2834-2868/Domain: LDL receptor ligand-binding repeat homology <LD16>
F;2874-2912/Domain: LDL receptor ligand-binding repeat homology <LD17>
F;2919-2956/Domain: LDL receptor ligand-binding repeat homology <LD18>
F;2961-2997/Domain: LDL receptor ligand-binding repeat homology <LD19>
F;3006-3044/Domain: LDL receptor ligand-binding repeat homology <LD20>
F;3049-3093/Domain: LDL receptor ligand-binding repeat homology <LD21>
F;3100-3135/Domain: LDL receptor ligand-binding repeat homology <LD22>
F;3140-3174/Domain: LDL receptor ligand-binding repeat homology <LD23>
F;3187-3222/Domain: LDL receptor ligand-binding repeat homology <LD24>
F;3586-3623/Domain: EGF homology <EGX1>
F;3627-3666/Domain: LDL receptor ligand-binding repeat homology <LD25>
F;3671-3705/Domain: LDL receptor ligand-binding repeat homology <LD26>
F;3709-3746/Domain: LDL receptor ligand-binding repeat homology <LD27>
F;3753-3788/Domain: LDL receptor ligand-binding repeat homology <LD28>
F;3793-3830/Domain: LDL receptor ligand-binding repeat homology <LD29>
F;3833-3871/Domain: LDL receptor ligand-binding repeat homology <LD30>
F;3878-3912/Domain: LDL receptor ligand-binding repeat homology <LD31>
F;3917-3951/Domain: LDL receptor ligand-binding repeat homology <LD32>
F;3959-3995/Domain: LDL receptor ligand-binding repeat homology <LD33>
F;4000-4040/Domain: LDL receptor ligand-binding repeat homology <LD34>
F;4049-4083/Domain: LDL receptor ligand-binding repeat homology <LD35>
F;4092-4130/Domain: EGF homology <EGF2>
F;4343-4386/Domain: LDL receptor YWTD-containing repeat homology <YW38>

  Query Match             66.2%;  Score 43;  DB 1;  Length 4753;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCF 8
              | | ||||
Db        361 CSCLGDCF 368


RESULT 6
S29216
neurotoxin Tx2 - spider (Phoneutria nigriventer)
C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29216
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venc
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29216
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-48 <COR>
C;Superfamily: curtatoxin

  Query Match             65.4%;  Score 42.5;  DB 2;  Length 48;
  Best Local Similarity   58.3%;  Pred. No. 7.2;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         14 CDCCGERGECVC 25


RESULT 7
S29215
neurotoxin Tx2 - spider (Phoneutria nigriventer)
C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Accession: S29215; B39305
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29215
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-49 <COR>
R;Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxicon 29, 1225-1233, 1991
A;Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria
A;Reference number: A39305; MUID:92196803; PMID:1801316
A;Accession: B39305
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <REZ>
C;Superfamily: curtatoxin
C;Keywords: neurotoxin; venom

  Query Match             65.4%;  Score 42.5;  DB 2;  Length 49;
  Best Local Similarity   58.3%;  Pred. No. 7.3;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         14 CDCCGERGECVC 25


RESULT 8
S29214
neurotoxin Tx2 - spider (Phoneutria nigriventer)
C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29214
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29214
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-53 <COR>
C;Superfamily: curtatoxin

  Query Match             65.4%;  Score 42.5;  DB 2;  Length 53;
  Best Local Similarity   58.3%;  Pred. No. 7.7;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         14 CDCCGERGECVC 25


RESULT 9
A55011
metallothionein-like protein YOR031w - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O2675
C;Species: Saccharomyces cerevisiae
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 19-Apr-2002
C;Accession: A55011; S66897
R;Culotta, V.C.; Howard, W.R.; Liu, X.F.
J. Biol. Chem. 269, 25295-25302, 1994
A;Title: CRS5 encodes a metallothionein-like protein in Saccharomyces cerevisiae.
```

A;Reference number: A55011; MUID:95014318; PMID:7929222
A;Accession: A55011
A;Molecule type: DNA
A;Residues: 1-69 <CUL>
A;Cross-references: GB:L29056; NID:g499891; PIDN:AAA66061.1; PID:g499892
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
A;Accession: S66897
A;Molecule type: DNA
A;Residues: 1-8 <DEH>
A;Cross-references: EMBL:Z74939; MIPS:YOR031w
A;Experimental source: strain S288C
A;Note: in strain S288C YOR031w is a pseudogene with an inframe stopcodon
C;Genetics:
A;Gene: SGD:CRS5; CRS5
A;Cross-references: SGD:S0005557
A;Map position: 15R
A;Note: YOR031w
C;Function:
A;Description: involved in copper homeostasis and detoxification

Query Match 63.1%; Score 41; DB 2; Length 69;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CDCRGDC 7
||| |:|
Db 6 CDCEGEC 12

RESULT 10
A84306
hypothetical protein Vng1524c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84306
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A84306
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: GB:AE004437; NID:g10581011; PIDN:AAG19813.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1524C
C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match 63.1%; Score 41; DB 2; Length 458;
Best Local Similarity 55.6%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | |:| |
Db 198 CTCEGECSC 206

RESULT 11
T06757
hypothetical protein F15B8.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06757
R;Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Salanoubat, M.; Mewes,
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15794
A;Accession: T06757
A;Molecule type: DNA
A;Residues: 1-736 <QUE>
A;Cross-references: EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.180
A;Experimental source: cultivar Columbia; BAC clone F15B8
C;Genetics:
A;Gene: ATSP:F15B8.180
A;Map position: 3
A;Introns: 114/3; 146/1; 208/2; 293/3; 365/3; 384/3; 429/3; 467/3; 536/2; 563/2; 640/3

Query Match 63.1%; Score 41; DB 2; Length 736;
Best Local Similarity 53.8%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

Qy 1 CDCRGDC----FC 9
||| : || ||
Db 257 CDCKYDCLWGRFC 269

RESULT 12
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T23433
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19740
A;Accession: T23433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3672 <WIL>
A;Cross-references: EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:K08C7.3
A;Experimental source: clone K08C7
C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like ho

Query Match 63.1%; Score 41; DB 2; Length 3672;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|| | |:|
Db 668 CDSNGQCYC 676

RESULT 13
T37316
probable laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T37316
R;Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: Z21681
A;Accession: T37316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3704 <JOH>
A;Cross-references: EMBL:AB016806; PIDN:BAA32347.1
A;Experimental source: strain N2
C;Genetics:
A;Gene: epi-1
A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like ho

Query Match 63.1%; Score 41; DB 2; Length 3704;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 CDCRGDCFC 9
              ||  |.|:|
Db        668 CDSNGQCYC 676


RESULT 14
TVVPA
small T antigen - mouse polyomavirus
C;Species: Polyomavirus muris (mouse polyomavirus)
C;Date: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 24-Sep-1999
C;Accession: C03635; B36761; C28838; A03614
R;Soeda, E.; Arrand, J.R.; Smolar, N.; Walsh, J.E.; Griffin, B.E.
Nature 283, 445-453, 1980
A;Title: Coding potential and regulatory signals of the polyoma virus genome.
A;Reference number: A03635; MUID:80099647; PMID:6243401
A;Accession: C03635
A;Molecule type: DNA
A;Residues: 1-195 <SOE>
A;Cross-references: GB:J02288; GB:J02290; GB:J02291; GB:J02292; GB:K00932; GB:K00997; GE
A;Experimental source: strain A2
R;Friedmann, T.; Esty, A.; LaPorte, P.; Deininger, P.
Cell 17, 715-724, 1979
A;Title: The nucleotide sequence and genome organization of the polyoma early region: ex
A;Reference number: A36761; MUID:80001963; PMID:225042
A;Accession: B36761
A;Molecule type: DNA
A;Residues: 1-195 <FRI>
A;Cross-references: GB:J02288; GB:J02290; GB:J02291; GB:J02292; GB:K00932; GB:K00997; GE
A;Experimental source: strain 3
R;Rothwell, V.M.; Folk, W.R.
J. Virol. 48, 472-480, 1983
A;Title: Comparison of the DNA sequence of the Crawford small-plaque variant of polyomav
A;Reference number: A28838; MUID:84011043; PMID:6312103
A;Accession: C28838
A;Molecule type: DNA
A;Residues: 1-195 <ROT>
A;Cross-references: GB:K02737; NID:g332788
A;Experimental source: strain Crawford small-plaque
A;Note: this ORF is not annotated in GenBank entry PLYCSP
C;Genetics:
A;Introns: 192/1
C;Superfamily: small T antigen; dnaJ amino-terminal homology
C;Keywords: early protein
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>

  Query Match             61.5%;  Score 40;  DB 1;  Length 195;
  Best Local Similarity   53.8%;  Pred. No. 47;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 CDCR----GDCFC 9
              || |    |:|||
Db        138 CDARCLVLGECFC 150


RESULT 15
S22562
small T antigen - mouse plasmid L factor
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: S22562
R;Yoshimura, H.; Ikeda, Y.; Yoshimoto, M.; Tamaki, S.; Hanada, K.; Kusano, T.; Kohda, T.
Nucleic Acids Res. 19, 3633-3639, 1991
A;Title: Structural and functional analysis of a polyoma-related mammalian plasmid (L fa
A;Reference number: S22560; MUID:91305109; PMID:1649455
A;Accession: S22562
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <YOS>
A;Cross-references: EMBL:X59849; NID:g52899; PIDN:CAA42512.1; PID:g52902
C;Genetics:
A;Genome: plasmid
A;Introns: 192/1
C;Superfamily: small T antigen; dnaJ amino-terminal homology
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>

  Query Match             61.5%;  Score 40;  DB 2;  Length 195;
  Best Local Similarity   53.8%;  Pred. No. 47;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 CDCR----GDCFC 9
              || |    |:|||
Db        138 CDARCLVLGECFC 150


Search completed: July 11, 2004, 09:17:02
Job time : 22 secs
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	67.7	577	1	ITB6_CAVPO	P18563 cavia porce
2	44	67.7	787	1	ITB6_MOUSE	Q9z0t9 mus musculu
3	44	67.7	788	1	ITB6_HUMAN	P18564 homo sapien
4	43	66.2	1627	1	PAPA_HUMAN	Q13219 homo sapien
5	43	66.2	4753	1	LRP_CAEEL	Q04833 caenorhabdi
6	42.5	65.4	49	1	TX25_PHONI	P29424 phoneutria
7	42.5	65.4	82	1	TX26_PHONI	P29425 phoneutria
8	42.5	65.4	82	1	TX5A_PHONI	O76199 phoneutria
9	42.5	65.4	88	1	TX21_PHONI	P29423 phoneutria
10	42.5	65.4	115	1	TX1A_PHONI	O76198 phoneutria
11	41	63.1	69	1	CRS5_YEAST	P41902 saccharomyc
12	41	63.1	3672	1	LML2_CAEEL	Q21313 caenorhabdi
13	40.5	62.3	799	1	ITBN_DROME	Q27591 drosophila
14	40	61.5	195	1	TASM_POVMA	P03078 mouse polyo
15	40	61.5	421	1	TAMI_POVMA	P03077 mouse polyo
16	40	61.5	421	1	TAMI_POVMC	P12906 mouse polyo
17	40	61.5	440	1	TAMI_POVM3	P03076 mouse polyo
18	39.5	60.8	246	1	AEG_RAT	P12020 rattus norv
19	39.5	60.8	423	1	TIC2_MOUSE	Q9er58 mus musculu
20	39	60.0	30	1	ITR1_MOMCH	P10294 momordica c
21	39	60.0	30	1	ITR3_MOMCO	P82410 momordica c
22	39	60.0	60	1	MTA_CHAAC	O93593 chaenocepha
23	39	60.0	60	1	MTA_CHIHA	O13258 chionodraco
24	39	60.0	60	1	MTA_NOTCO	O73914 notothenia
25	39	60.0	60	1	MTA_PAGBE	O93609 pagothenia
26	39	60.0	60	1	MTA_SPAAU	P52727 sparus aura
27	39	60.0	60	1	MTB_CHAAC	P52724 chaenocepha
28	39	60.0	60	1	MTB_CHIHA	O13259 chionodraco
29	39	60.0	60	1	MTB_DICLA	Q9ptg9 dicentrarch
30	39	60.0	60	1	MTB_PAGBE	Q92145 pagothenia
31	39	60.0	60	1	MT_OREMO	P52726 oreochromis
32	39	60.0	60	1	MT_PAGMA	Q9ib50 pagrus majo
33	39	60.0	60	1	MT_PARCR	O93450 parachaenic
34	39	60.0	60	1	MT_PERFL	P52725 perca fluvi
35	39	60.0	60	1	MT_PLEPL	P07216 pleuronecte
36	39	60.0	60	1	MT_PSEAM	P55945 pseudopleur
37	39	60.0	61	1	MT1A_BOVIN	P04356 bos taurus
38	39	60.0	61	1	MT1A_PIG	P49068 sus scrofa
39	39	60.0	61	1	MT1B_SHEEP	P09577 ovis aries
40	39	60.0	61	1	MT1C_PIG	P79376 sus scrofa
41	39	60.0	61	1	MT1C_SHEEP	P09578 ovis aries
42	39	60.0	61	1	MT1E_PIG	P79431 sus scrofa
43	39	60.0	65	1	MT_PARLI	P80367 paracentrot
44	39	60.0	68	1	MT3_HORSE	P37360 equus cabal
45	39	60.0	624	1	SUV4_ARATH	Q8gzb6 arabidopsis

ALIGNMENTS

RESULT 1
ITB6_CAVPO
ID ITB6_CAVPO STANDARD; PRT; 577 AA.
AC P18563;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Integrin beta-6 (Fragment).
GN ITGB6.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RX MEDLINE=90307659; PubMed=2365683;
RA Sheppard D., Rozzo C., Starr L., Quaranta V., Erle D.J., Pytela R.;
RT "Complete amino acid sequence of a novel integrin beta subunit (beta
RT 6) identified in epithelial cells using the polymerase chain
RT reaction.";
RL J. Biol. Chem. 265:11502-11507(1990).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN
CC AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-6
CC associates with alpha-V. Interacts with FLNB (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the integrin beta chain family.
CC -!- SIMILARITY: Contains 2 VWFA-like domains.
CC --

CC --
DR EMBL; M35197; AAA37043.1; -.
DR EMBL; A26611; CAA01833.1; -.
DR PIR; B37057; B37057.
DR HSSP; P05106; 1JV2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR Pfam; PF00362; integrin_B; 1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR PROSITE; PS00243; INTEGRIN_BETA; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat.
FT NON_TER 1 1
FT DOMAIN <1 566 EXTRACELLULAR (POTENTIAL).

```
FT   TRANSMEM    567   >577       POTENTIAL.
FT   DOMAIN       <1    230       VWFA-LIKE.
FT   DOMAIN      315    478       4 CYSTEINE-RICH TANDEM REPEATS.
FT   REPEAT      315    360       I.
FT   REPEAT      361    402       II.
FT   REPEAT      403    441       III.
FT   REPEAT      442    478       IV.
FT   DISULFID     56     63       BY SIMILARITY.
FT   DISULFID    111    152       BY SIMILARITY.
FT   DISULFID    253    265       BY SIMILARITY.
FT   DISULFID    285    529       BY SIMILARITY.
FT   DISULFID    311    315       BY SIMILARITY.
FT   DISULFID    326    338       BY SIMILARITY.
FT   DISULFID    335    370       BY SIMILARITY.
FT   DISULFID    340    349       BY SIMILARITY.
FT   DISULFID    351    361       BY SIMILARITY.
FT   DISULFID    376    381       BY SIMILARITY.
FT   DISULFID    378    411       BY SIMILARITY.
FT   DISULFID    383    396       BY SIMILARITY.
FT   DISULFID    398    403       BY SIMILARITY.
FT   DISULFID    417    422       BY SIMILARITY.
FT   DISULFID    419    450       BY SIMILARITY.
FT   DISULFID    424    433       BY SIMILARITY.
FT   DISULFID    435    442       BY SIMILARITY.
FT   DISULFID    456    461       BY SIMILARITY.
FT   DISULFID    458    504       BY SIMILARITY.
FT   DISULFID    463    473       BY SIMILARITY.
FT   DISULFID    476    479       BY SIMILARITY.
FT   DISULFID    483    492       BY SIMILARITY.
FT   DISULFID    489    561       BY SIMILARITY.
FT   DISULFID    508    537       BY SIMILARITY.
FT   CARBOHYD    119    119       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    277    277       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    322    322       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    330    330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    400    400       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    555    555       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     577    577
SQ   SEQUENCE   577 AA;  62298 MW;  B83B468C83EDCCF9 CRC64;

  Query Match             67.7%;  Score 44;  DB 1;  Length 577;
  Best Local Similarity   66.7%;  Pred. No. 7.5;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        370 CSGRGDCYC 378


RESULT 2
ITB6_MOUSE
ID   ITB6_MOUSE     STANDARD;      PRT;   787 AA.
AC   Q9Z0T9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Integrin beta-6 precursor.
GN   ITGB6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=20547423; PubMed=11095652;
RA   Arend L.J., Smart A.M., Briggs J.P.;
RT   "Mouse beta(6) integrin sequence, pattern of expression, and role in
RT   kidney development.";
RL   J. Am. Soc. Nephrol. 11:2297-2305(2000).
CC   -!- FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN
CC       AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-6
CC       associates with alpha-V. Interacts with FLNB (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the integrin beta chain family.
CC   -!- SIMILARITY: Contains 2 VWFA-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF115376; AAD17212.1; -.
DR   HSSP; P05106; 1JV2.
DR   MGD; MGI:96615; Itgb6.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   InterPro; IPR001169; Integrin_beta_C.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF00362; integrin_B; 1.
DR   PRINTS; PR01186; INTEGRINB.
DR   ProDom; PD001811; Integrin_B; 1.
DR   SMART; SM00187; INB; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00243; INTEGRIN_BETA; 2.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW   Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW   Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    787       INTEGRIN BETA-6.
FT   DOMAIN       22    706       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    707    729       POTENTIAL.
FT   DOMAIN      730    787       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      131    371       VWFA-LIKE.
FT   DOMAIN      456    619       4 CYSTEINE-RICH TANDEM REPEATS.
FT   REPEAT      456    501       I.
FT   REPEAT      502    543       II.
FT   REPEAT      544    582       III.
FT   REPEAT      583    619       IV.
FT   DISULFID     23    454       BY SIMILARITY.
FT   DISULFID     31     41       BY SIMILARITY.
FT   DISULFID     34     70       BY SIMILARITY.
FT   DISULFID     44     59       BY SIMILARITY.
FT   DISULFID    197    204       BY SIMILARITY.
FT   DISULFID    252    293       BY SIMILARITY.
FT   DISULFID    394    406       BY SIMILARITY.
FT   DISULFID    426    669       BY SIMILARITY.
FT   DISULFID    452    456       BY SIMILARITY.
FT   DISULFID    467    479       BY SIMILARITY.
FT   DISULFID    476    511       BY SIMILARITY.
FT   DISULFID    481    490       BY SIMILARITY.
FT   DISULFID    492    502       BY SIMILARITY.
FT   DISULFID    517    522       BY SIMILARITY.
FT   DISULFID    519    552       BY SIMILARITY.
FT   DISULFID    524    537       BY SIMILARITY.
FT   DISULFID    539    544       BY SIMILARITY.
FT   DISULFID    558    563       BY SIMILARITY.
FT   DISULFID    560    591       BY SIMILARITY.
FT   DISULFID    565    574       BY SIMILARITY.
FT   DISULFID    576    583       BY SIMILARITY.
FT   DISULFID    597    602       BY SIMILARITY.
FT   DISULFID    599    645       BY SIMILARITY.
FT   DISULFID    604    614       BY SIMILARITY.
FT   DISULFID    617    620       BY SIMILARITY.
FT   DISULFID    624    633       BY SIMILARITY.
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FT   DISULFID    630    701       BY SIMILARITY.
FT   DISULFID    649    677       BY SIMILARITY.
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    387    387       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    418    418       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    471    471       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    541    541       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    575    575       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   787 AA;  86041 MW;  C6438C6F1E6B7FBD CRC64;

  Query Match             67.7%;  Score 44;  DB 1;  Length 787;
  Best Local Similarity   66.7%;  Pred. No. 10;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        511 CSGRGDCYC 519


RESULT 3
ITB6_HUMAN
ID   ITB6_HUMAN     STANDARD;      PRT;   788 AA.
AC   P18564; Q16500;
DT   01-NOV-1990 (Rel. 16, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Integrin beta-6 precursor.
GN   ITGB6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=90307659; PubMed=2365683;
RA   Sheppard D., Rozzo C., Starr L., Quaranta V., Erle D.J., Pytela R.;
RT   "Complete amino acid sequence of a novel integrin beta subunit (beta
RT   6) identified in epithelial cells using the polymerase chain
RT   reaction.";
RL   J. Biol. Chem. 265:11502-11507(1990).
RN   [2]
RP   REVISIONS TO 18-24; 158; 642 AND 719.
RA   Askins J.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 116-197 FROM N.A.
RX   MEDLINE=93002753; PubMed=1382574;
RA   Jiang W.M., Jenkins D., Yuan Q., Leung E., Choo K.H., Watson J.D.,
RA   Krissansen G.W.;
RT   "The gene organization of the human beta 7 subunit, the common beta
RT   subunit of the leukocyte integrins HML-1 and LPAM-1.";
RL   Int. Immunol. 4:1031-1040(1992).
RN   [4]
RP   INTERACTION WITH FLNB.
RC   TISSUE=Keratinocytes, and Skeletal muscle;
RX   PubMed=11807098;
RA   Van der Flier A., Kuikman I., Kramer D., Geerts D., Kreft M.,
RA   Takafuta T., Shapiro S.S., Sonnenberg A.;
RT   "Different splice variants of filamin-B affect myogenesis, subcellular
RT   distribution, and determine binding to integrin (beta) subunits.";
RL   J. Cell Biol. 156:361-376(2002).
CC   -!- FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN
CC       AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS.
CC   -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-6
CC       associates with alpha-V. Interacts with FLNB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the integrin beta chain family.
CC   -!- SIMILARITY: Contains 2 VWFA-like domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M35198; AAA36122.2; -.
DR   EMBL; A26609; CAA01832.1; -.
DR   EMBL; S49380; AAB23690.1; -.
DR   PIR; A37057; A37057.
DR   PDB; 1LH9; 15-MAY-02.
DR   Genew; HGNC:6161; ITGB6.
DR   MIM; 147558; -.
DR   GO; GO:0008305; C:integrin complex; TAS.
DR   GO; GO:0004895; F:cell adhesion receptor activity; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   InterPro; IPR001169; Integrin_beta_C.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF00362; integrin_B; 1.
DR   PRINTS; PR01186; INTEGRINB.
DR   ProDom; PD001811; Integrin_B; 1.
DR   SMART; SM00187; INB; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00243; INTEGRIN_BETA; 3.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW   Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW   Repeat; Signal; 3D-structure.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    788       INTEGRIN BETA-6.
FT   DOMAIN       22    707       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    708    730       POTENTIAL.
FT   DOMAIN      731    788       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      131    371       VWFA-LIKE.
FT   DOMAIN      456    619       4 CYSTEINE-RICH TANDEM REPEATS.
FT   REPEAT      456    501       I.
FT   REPEAT      502    543       II.
FT   REPEAT      544    582       III.
FT   REPEAT      583    619       IV.
FT   DISULFID     23    454       BY SIMILARITY.
FT   DISULFID     31     41       BY SIMILARITY.
FT   DISULFID     34     70       BY SIMILARITY.
FT   DISULFID     44     59       BY SIMILARITY.
FT   DISULFID    197    204       BY SIMILARITY.
FT   DISULFID    252    293       BY SIMILARITY.
FT   DISULFID    394    406       BY SIMILARITY.
FT   DISULFID    426    670       BY SIMILARITY.
FT   DISULFID    452    456       BY SIMILARITY.
FT   DISULFID    467    479       BY SIMILARITY.
FT   DISULFID    476    511       BY SIMILARITY.
FT   DISULFID    481    490       BY SIMILARITY.
FT   DISULFID    492    502       BY SIMILARITY.
FT   DISULFID    517    522       BY SIMILARITY.
FT   DISULFID    519    552       BY SIMILARITY.
FT   DISULFID    524    537       BY SIMILARITY.
FT   DISULFID    539    544       BY SIMILARITY.
FT   DISULFID    558    563       BY SIMILARITY.
FT   DISULFID    560    591       BY SIMILARITY.
FT   DISULFID    565    574       BY SIMILARITY.
FT   DISULFID    576    583       BY SIMILARITY.
FT   DISULFID    597    602       BY SIMILARITY.
FT   DISULFID    599    645       BY SIMILARITY.
FT   DISULFID    604    614       BY SIMILARITY.
FT   DISULFID    617    620       BY SIMILARITY.
FT   DISULFID    624    633       BY SIMILARITY.
FT   DISULFID    630    702       BY SIMILARITY.
FT   DISULFID    649    678       BY SIMILARITY.
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    387    387       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    396    396       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    471    471       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    541    541       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    575    575       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   788 AA;  85935 MW;  EDB7D533EC4C8C4D CRC64;

  Query Match             67.7%;  Score 44;  DB 1;  Length 788;
  Best Local Similarity   66.7%;  Pred. No. 10;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        511 CSGRGDCYC 519


RESULT 4
PAPA_HUMAN
ID   PAPA_HUMAN     STANDARD;      PRT;  1627 AA.
AC   Q13219; Q08371; Q9UDK7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Pappalysin-1 precursor (EC 3.4.24.79) (Pregnancy-associated plasma
DE   protein-A) (PAPP-A) (Insulin-like growth factor-dependent IGF binding
DE   protein-4 protease) (IGF-dependent IGFBP-4 protease) (IGFBP-4ase).
GN   PAPPA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND INDUCTION.
RC   TISSUE=Placenta;
RX   MEDLINE=96203921; PubMed=8620868;
RA   Haaning J., Oxvig C., Overgaard M.T., Ebbesen P., Kristensen T.,
RA   Sottrup-Jensen L.;
RT   "Complete cDNA sequence of the preproform of human pregnancy-
RT   associated plasma protein-A. Evidence for expression in the brain and
RT   induction by cAMP.";
RL   Eur. J. Biochem. 237:159-163(1996).
RN   [2]
RP   SEQUENCE OF 77-1627 FROM N.A., SEQUENCE OF 81-98; 117-126; 210-224;
RP   466-485; 507-519; 576-593; 609-621; 718-736; 742-754; 1006-1017;
RP   1259-1273; 1369-1374; 1389-1398; 1490-1509; 1524-1533 AND 1537-1544,
RP   VARIANT SER-944, AND TISSUE SPECIFICITY.
RC   TISSUE=Placenta, and Serum;
RX   MEDLINE=94146014; PubMed=7508748;
RA   Kristensen T., Oxvig C., Sand O., Moller N.P.H., Sottrup-Jensen L.;
RT   "Amino acid sequence of human pregnancy-associated plasma protein-A
RT   derived from cloned cDNA.";
RL   Biochemistry 33:1592-1598(1994).
RN   [3]
RP   SEQUENCE OF 81-89; 117-126; 210-224; 460-485; 507-519; 576-593;
RP   718-736; 742-754; 1259-1273; 1369-1374; 1490-1509; 1524-1533 AND
RP   1537-1544, SUBUNITS, AND INTERCHAIN DISULFIDE BOND.
RC   TISSUE=Serum;
RX   MEDLINE=93286045; PubMed=7685339;
RA   Oxvig C., Sand O., Kristensen T., Gleich G.J., Sottrup-Jensen L.;
RT   "Circulating human pregnancy-associated plasma protein-A is disulfide-
RT   bridged to the proform of eosinophil major basic protein.";
RL   J. Biol. Chem. 268:12243-12246(1993).
RN   [4]
RP   PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX   MEDLINE=22421368; PubMed=12421832;
RA   Overgaard M.T., Sorensen E.S., Stachowiak D., Boldt H.B.,
RA   Kristensen L., Sottrup-Jensen L., Oxvig C.;
RT   "Complex of pregnancy-associated plasma protein-A and the proform of
RT   eosinophil major basic protein. Disulfide structure and carbohydrate
RT   attachment sites.";
RL   J. Biol. Chem. 278:2106-2117(2003).
RN   [5]
RP   IDENTIFICATION, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP   SPECIFICITY.
RC   TISSUE=Fibroblast;
RX   MEDLINE=99179030; PubMed=10077652;
RA   Lawrence J.B., Oxvig C., Overgaard M.T., Sottrup-Jensen L.,
RA   Gleich G.J., Hays L.G., Yates J.R. III, Conover C.A.;
RT   "The insulin-like growth factor (IGF)-dependent IGF binding protein-4
RT   protease secreted by human fibroblasts is pregnancy-associated plasma
RT   protein-A.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:3149-3153(1999).
RN   [6]
RP   FUNCTION, SUBUNITS, AND ENZYME REGULATION.
RX   MEDLINE=20469470; PubMed=10913121;
RA   Overgaard M.T., Haaning J., Boldt H.B., Olsen I.M., Laursen L.S.,
RA   Christiansen M., Gleich G.J., Sottrup-Jensen L., Conover C.A.,
RA   Oxvig C.;
RT   "Expression of recombinant human pregnancy-associated plasma protein-A
RT   and identification of the proform of eosinophil major basic protein
RT   as its physiological inhibitor.";
RL   J. Biol. Chem. 275:31128-31133(2000).
RN   [7]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=95057018; PubMed=7526035;
RA   Bonno M., Oxvig C., Kephart G.M., Wagner J.M., Kristensen T.,
RA   Sottrup-Jensen L., Gleich G.J.;
RT   "Localization of pregnancy-associated plasma protein-A and
RT   colocalization of pregnancy-associated plasma protein-A messenger
RT   ribonucleic acid and eosinophil granule major basic protein messenger
RT   ribonucleic acid in placenta.";
RL   Lab. Invest. 71:560-566(1994).
RN   [8]
RP   TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=99423540; PubMed=10491647;
RA   Overgaard M.T., Oxvig C., Christiansen M., Lawrence J.B.,
RA   Conover C.A., Gleich G.J., Sottrup-Jensen L., Haaning J.;
RT   "Messenger ribonucleic acid levels of pregnancy-associated plasma
RT   protein-A and the proform of eosinophil major basic protein:
RT   expression in human reproductive and nonreproductive tissues.";
RL   Biol. Reprod. 61:1083-1089(1999).
RN   [9]
RP   DEVELOPMENTAL STAGE.
RX   MEDLINE=95293954; PubMed=7539791;
RA   Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA   Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT   "Identification of angiotensinogen and complement C3dg as novel
RT   proteins binding the proform of eosinophil major basic protein in
RT   human pregnancy serum and plasma.";
RL   J. Biol. Chem. 270:13645-13651(1995).
CC   -!- FUNCTION: Metalloproteinase which specifically cleaves IGFBP-4 in
CC       the presence of IGF, resulting in release of bound IGF.
CC   -!- CATALYTIC ACTIVITY: Cleavage of the 135-Met-|-Lys-136 bond in
CC       insulin-like growth factor binding protein (IGFBP)-4, and the 143-
CC       Ser-|-Lys-144 bond in IGFBP-5.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by complexation with the proform
CC       of PRG2.
CC   -!- SUBUNIT: Homodimer; disulfide-linked. In pregnancy serum,
CC       predominantly found as a disulfide-linked 2:2 heterotetramer with
CC       the proform of PRG2.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: High levels in placenta and pregnancy serum.
CC       In placenta, expressed in X cells in septa and anchoring villi,
CC       and in syncytiotrophoblasts in the chorionic villi. Lower levels
CC       are found in a variety of other tissues including kidney,
CC       myometrium, endometrium, ovaries, breast, prostate, bone marrow,
CC       colon, fibroblasts and osteoblasts.
CC   -!- DEVELOPMENTAL STAGE: Present in serum and placenta during
CC       pregnancy; levels increase throughout pregnancy.
CC   -!- INDUCTION: By 8-bromoadenosine-3',5'-phosphate.
CC   -!- PTM: There appear to be no free sulfhydryl groups.
CC   -!- SIMILARITY: Contains 5 Sushi (SCR) domains.
CC   -!- SIMILARITY: Belongs to peptidase family M43B.
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CC   ---------------------------------------------------------------------
DR   EMBL; U28727; AAC50543.1; -.
DR   EMBL; X68280; CAA48341.1; -.
DR   PIR; S65464; S65464.
DR   MEROPS; M43.004; -.
DR   Genew; HGNC:8602; PAPPA.
DR   MIM; 176385; -.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0008237; F:metallopeptidase activity; IDA.
DR   GO; GO:0008270; F:zinc ion binding; NAS.
DR   GO; GO:0007565; P:pregnancy; NAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006558; LamG_like.
DR   InterPro; IPR000800; Notch_dom.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR008754; Peptidase_M43B.
DR   InterPro; IPR000436; Sushi_SCR_CCP.
DR   Pfam; PF05572; Peptidase_M46; 1.
DR   Pfam; PF00084; sushi; 4.
DR   SMART; SM00032; CCP; 4.
DR   SMART; SM00560; LamGL; 1.
DR   SMART; SM00004; NL; 3.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Metal-binding; Zinc; Signal; Glycoprotein;
KW   Zymogen; Repeat; Sushi.
FT   SIGNAL       1     22       POTENTIAL.
FT   PROPEP      23     80
FT   CHAIN       81   1627       PAPPALYSIN-1.
FT   DOMAIN      24     83       ARG-RICH.
FT   DOMAIN     272    583       PROTEOLYTIC.
FT   DOMAIN    1215   1280       SUSHI 1.
FT   DOMAIN    1285   1342       SUSHI 2.
FT   DOMAIN    1346   1410       SUSHI 3.
FT   DOMAIN    1415   1471       SUSHI 4.
FT   DOMAIN    1478   1554       SUSHI 5.
FT   METAL      562    562       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE   563    563       BY SIMILARITY.
FT   METAL      566    566       ZINC (CATALYTIC) (BY SIMILARITY).
FT   DISULFID   144    235
FT   DISULFID   327    622
FT   DISULFID   332    657
FT   DISULFID   414    428
FT   DISULFID   424    440
FT   DISULFID   457    473
FT   DISULFID   461    461       INTERCHAIN (WITH C-51 IN PRG2 PROFORM).
FT   DISULFID   474    485
FT   DISULFID   583    600       OR 583-612.
FT   DISULFID   587    612       OR 587-600.
FT   DISULFID   710    878
FT   DISULFID   713    881
FT   DISULFID   732    732       INTERCHAIN (WITH C-169 IN PRG2 PROFORM).
FT   DISULFID   753    835
FT   DISULFID   775    781
FT   DISULFID   947    975
FT   DISULFID   960    971
FT   DISULFID   983    990
FT   DISULFID   999   1011
FT   DISULFID  1036   1070
FT   DISULFID  1051   1139
FT   DISULFID  1192   1205
FT   DISULFID  1210   1210       INTERCHAIN.
FT   DISULFID  1215   1269
FT   DISULFID  1227   1238
FT   DISULFID  1242   1280
FT   DISULFID  1285   1329
FT   DISULFID  1300   1310

  Query Match             66.2%;  Score 43;  DB 1;  Length 1627;
  Best Local Similarity   66.7%;  Pred. No. 28;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              || :||| |
Db       1600 CDLQGDCAC 1608


RESULT 5
LRP_CAEEL
ID   LRP_CAEEL      STANDARD;      PRT;  4753 AA.
AC   Q04833;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Low-density lipoprotein receptor-related protein precursor (LRP).
GN   LRP-1 OR F29D11.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93281621; PubMed=8506301;
RA   Yochem J., Greenwald I.;
RT   "A gene for a low density lipoprotein receptor-related protein in the
RT   nematode Caenorhabditis elegans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:4572-4576(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilkinson J.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May act as a receptor for the endocytosis of
CC       extracellular ligands such as chylomicron remnants, protease-
CC       inhibitor complexes and vitellogenin.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 35 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 17 EGF-like domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M96150; AAA28105.1; -.
DR   EMBL; Z73907; CAA98124.1; -.
DR   PIR; A47437; A47437.
DR   HSSP; Q07954; 1CR8.
DR   WormPep; F29D11.1; CE05765.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   Pfam; PF00057; ldl_recept_a; 34.
DR   Pfam; PF00058; ldl_recept_b; 26.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00179; EGF_CA; 2.
DR   SMART; SM00192; LDLa; 35.
DR   SMART; SM00135; LY; 32.
DR   PROSITE; PS00010; ASX_HYDROXYL; 6.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS50026; EGF_3; 2.
DR   PROSITE; PS01187; EGF_CA; 3.
DR   PROSITE; PS01209; LDLRA_1; 27.
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DR   PROSITE; PS50068; LDLRA_2; 34.
KW   Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein;
KW   Signal; Calcium-binding; EGF-like domain; Coated pits.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19   4753       LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
FT                                PROTEIN.
FT   DOMAIN       19   4570       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   4571   4596       POTENTIAL.
FT   DOMAIN     4597   4753       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       51     89       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN       90    133       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN      136    177       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN      180    220       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN      221    259       LDL-RECEPTOR CLASS A 5.
FT   DOMAIN      260    298       LDL-RECEPTOR CLASS A 6.
FT   DOMAIN      299    337       EGF-LIKE 1.
FT   DOMAIN      338    368       EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN      669    712       EGF-LIKE 3.
FT   DOMAIN      997   1043       EGF-LIKE 4.
FT   DOMAIN     1052   1097       LDL-RECEPTOR CLASS A 7.
FT   DOMAIN     1099   1140       LDL-RECEPTOR CLASS A 8.
FT   DOMAIN     1144   1184       LDL-RECEPTOR CLASS A 9.
FT   DOMAIN     1185   1225       LDL-RECEPTOR CLASS A 10.
FT   DOMAIN     1226   1265       LDL-RECEPTOR CLASS A 11.
FT   DOMAIN     1268   1309       LDL-RECEPTOR CLASS A 12.
FT   DOMAIN     1311   1352       LDL-RECEPTOR CLASS A 13.
FT   DOMAIN     1357   1397       LDL-RECEPTOR CLASS A 14.
FT   DOMAIN     1398   1436       EGF-LIKE 5.
FT   DOMAIN     1437   1476       EGF-LIKE 6.
FT   DOMAIN     1747   1786       EGF-LIKE 7.
FT   DOMAIN     2080   2120       EGF-LIKE 8.
FT   DOMAIN     2396   2439       EGF-LIKE 9.
FT   DOMAIN     2728   2780       EGF-LIKE 10.
FT   DOMAIN     2790   2831       LDL-RECEPTOR CLASS A 15.
FT   DOMAIN     2832   2870       LDL-RECEPTOR CLASS A 16.
FT   DOMAIN     2872   2914       LDL-RECEPTOR CLASS A 17.
FT   DOMAIN     2917   2958       LDL-RECEPTOR CLASS A 18.
FT   DOMAIN     2959   2999       LDL-RECEPTOR CLASS A 19.
FT   DOMAIN     3004   3046       LDL-RECEPTOR CLASS A 20.
FT   DOMAIN     3047   3095       LDL-RECEPTOR CLASS A 21.
FT   DOMAIN     3098   3137       LDL-RECEPTOR CLASS A 22.
FT   DOMAIN     3138   3176       LDL-RECEPTOR CLASS A 23.
FT   DOMAIN     3185   3223       LDL-RECEPTOR CLASS A 24.
FT   DOMAIN     3224   3265       EGF-LIKE 11.
FT   DOMAIN     3266   3306       EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     3582   3624       EGF-LIKE 13.
FT   DOMAIN     3625   3668       LDL-RECEPTOR CLASS A 25.
FT   DOMAIN     3669   3707       LDL-RECEPTOR CLASS A 26.
FT   DOMAIN     3707   3748       LDL-RECEPTOR CLASS A 27.
FT   DOMAIN     3751   3790       LDL-RECEPTOR CLASS A 28.
FT   DOMAIN     3791   3832       LDL-RECEPTOR CLASS A 29.
FT   DOMAIN     3831   3873       LDL-RECEPTOR CLASS A 30.
FT   DOMAIN     3876   3914       LDL-RECEPTOR CLASS A 31.
FT   DOMAIN     3915   3953       LDL-RECEPTOR CLASS A 32.
FT   DOMAIN     3957   3997       LDL-RECEPTOR CLASS A 33.
FT   DOMAIN     3998   4042       LDL-RECEPTOR CLASS A 34.
FT   DOMAIN     4047   4085       LDL-RECEPTOR CLASS A 35.
FT   DOMAIN     4088   4131       EGF-LIKE 14.
FT   DOMAIN     4132   4176       EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     4477   4515       EGF-LIKE 16.
FT   DOMAIN     4526   4554       EGF-LIKE 17.
FT   SITE       4653   4658       ENDOCYTOSIS SIGNAL (POTENTIAL).
FT   SITE       4744   4744       CRITICAL FOR ENDOCYTOSIS (BY SIMILARITY).
FT   DISULFID     53     65       BY SIMILARITY.
FT   DISULFID     60     78       BY SIMILARITY.
FT   DISULFID     72     87       BY SIMILARITY.
FT   DISULFID     92    109       BY SIMILARITY.
FT   DISULFID     99    122       BY SIMILARITY.
FT   DISULFID    116    131       BY SIMILARITY.
FT   DISULFID    138    152       BY SIMILARITY.
FT   DISULFID    146    165       BY SIMILARITY.
FT   DISULFID    159    175       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    189    208       BY SIMILARITY.
FT   DISULFID    202    218       BY SIMILARITY.
FT   DISULFID    223    235       BY SIMILARITY.
FT   DISULFID    230    248       BY SIMILARITY.
FT   DISULFID    242    257       BY SIMILARITY.
FT   DISULFID    262    275       BY SIMILARITY.
FT   DISULFID    269    288       BY SIMILARITY.
FT   DISULFID    282    297       BY SIMILARITY.
FT   DISULFID    302    311       BY SIMILARITY.
FT   DISULFID    307    320       BY SIMILARITY.
FT   DISULFID    322    336       BY SIMILARITY.
FT   DISULFID    342    352       BY SIMILARITY.
FT   DISULFID    348    361       BY SIMILARITY.
FT   DISULFID    363    367       BY SIMILARITY.
FT   DISULFID    673    682       BY SIMILARITY.
FT   DISULFID    678    697       BY SIMILARITY.
FT   DISULFID    699    711       BY SIMILARITY.
FT   DISULFID   1001   1010       BY SIMILARITY.
FT   DISULFID   1006   1026       BY SIMILARITY.
FT   DISULFID   1028   1042       BY SIMILARITY.
FT   DISULFID   1054   1068       BY SIMILARITY.
FT   DISULFID   1063   1081       BY SIMILARITY.
FT   DISULFID   1075   1095       BY SIMILARITY.
FT   DISULFID   1101   1114       BY SIMILARITY.
FT   DISULFID   1108   1127       BY SIMILARITY.
FT   DISULFID   1121   1138       BY SIMILARITY.
FT   DISULFID   1146   1158       BY SIMILARITY.
FT   DISULFID   1153   1171       BY SIMILARITY.
FT   DISULFID   1165   1182       BY SIMILARITY.
FT   DISULFID   1187   1199       BY SIMILARITY.
FT   DISULFID   1194   1212       BY SIMILARITY.
FT   DISULFID   1206   1223       BY SIMILARITY.
FT   DISULFID   1228   1241       BY SIMILARITY.
FT   DISULFID   1235   1254       BY SIMILARITY.
FT   DISULFID   1248   1263       BY SIMILARITY.
FT   DISULFID   1270   1283       BY SIMILARITY.
FT   DISULFID   1277   1296       BY SIMILARITY.
FT   DISULFID   1290   1307       BY SIMILARITY.
FT   DISULFID   1313   1325       BY SIMILARITY.
FT   DISULFID   1320   1338       BY SIMILARITY.
FT   DISULFID   1332   1350       BY SIMILARITY.
FT   DISULFID   1359   1373       BY SIMILARITY.
FT   DISULFID   1366   1386       BY SIMILARITY.
FT   DISULFID   1380   1396       BY SIMILARITY.
FT   DISULFID   1401   1412       BY SIMILARITY.
FT   DISULFID   1408   1421       BY SIMILARITY.
FT   DISULFID   1423   1435       BY SIMILARITY.
FT   DISULFID   1441   1451       BY SIMILARITY.
FT   DISULFID   1447   1460       BY SIMILARITY.
FT   DISULFID   1462   1475       BY SIMILARITY.
FT   DISULFID   1751   1760       BY SIMILARITY.
FT   DISULFID   1756   1770       BY SIMILARITY.
FT   DISULFID   1772   1785       BY SIMILARITY.
FT   DISULFID   2084   2095       BY SIMILARITY.
FT   DISULFID   2091   2105       BY SIMILARITY.
FT   DISULFID   2107   2119       BY SIMILARITY.
FT   DISULFID   2400   2415       BY SIMILARITY.
FT   DISULFID   2411   2426       BY SIMILARITY.
FT   DISULFID   2428   2438       BY SIMILARITY.
FT   DISULFID   2732   2743       BY SIMILARITY.
FT   DISULFID   2739   2759       BY SIMILARITY.
FT   DISULFID   2761   2779       BY SIMILARITY.
FT   DISULFID   2792   2805       BY SIMILARITY.
FT   DISULFID   2800   2818       BY SIMILARITY.
FT   DISULFID   2812   2829       BY SIMILARITY.
FT   DISULFID   2834   2846       BY SIMILARITY.
FT   DISULFID   2841   2859       BY SIMILARITY.

  Query Match           66.2%;  Score 43;  DB 1;  Length 4753;
  Best Local Similarity  75.0%;  Pred. No. 77;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCF 8
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                | | ||||
Db        361 CSCLGDCF 368


RESULT 6
TX25_PHONI
ID   TX25_PHONI     STANDARD;      PRT;    49 AA.
AC   P29424;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neurotoxin Tx2-5.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=93011905; PubMed=1397265;
RA   Cordeiro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA   Gilroy J., Richardson M.;
RT   "The purification and amino acid sequences of four Tx2 neurotoxins
RT   from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT   (Keys).";
RL   FEBS Lett. 310:153-156(1992).
RN   [2]
RP   SEQUENCE OF 1-10.
RC   TISSUE=Venom;
RX   MEDLINE=92196803; PubMed=1801316;
RA   Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;
RT   "Isolation of neurotoxic peptides from the venom of the 'armed'
RT   spider Phoneutria nigriventer.";
RL   Toxicon 29:1225-1233(1991).
CC   -!- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,
CC       lacrimation, hypersalivation, sweating and agitation followed by
CC       spastic paralysis of the anterior and posterior extremities and
CC       death at dose levels of 0.24 mg/mouse. Insecticidal to the larval
CC       and adult forms of the house fly.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
DR   PIR; S29215; S29215.
KW   Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor.
SQ   SEQUENCE   49 AA;  5111 MW;  77B46AAAB3911716 CRC64;

  Query Match             65.4%;  Score 42.5;  DB 1;  Length 49;
  Best Local Similarity   58.3%;  Pred. No. 1.3;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         14 CDCCGERGECVC 25


RESULT 7
TX26_PHONI
ID   TX26_PHONI     STANDARD;      PRT;    82 AA.
AC   P29425; Q95UF2;
DT   01-APR-1993 (Rel. 25, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neurotoxin Tx2-6 precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Penaforte C.L., Kalapothakis E.;
RT   "Molecular cloning of Tx2-6, a neurotoxin from the spider Phoneutria
RT   nigriventer.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 35-82 FROM N.A.
RC   TISSUE=Venom;
RX   MEDLINE=93011905; PubMed=1397265;
RA   Cordeiro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA   Gilroy J., Richardson M.;
RT   "The purification and amino acid sequences of four Tx2 neurotoxins
RT   from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT   (Keys).";
RL   FEBS Lett. 310:153-156(1992).
CC   -!- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,
CC       lacrimation, hypersalivation, sweating and agitation followed by
CC       spastic paralysis of the anterior and posterior extremities and
CC       death at dose levels of 0.79 mg/mouse. It significantly activates
CC       voltage-dependent sodium channels. Insecticidal to the larval and
CC       adult forms of the house fly.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AY054746; AAL14349.1; -.
DR   PIR; S29216; S29216.
KW   Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     34
FT   CHAIN        35     81       NEUROTOXIN TX2-6.
FT   PROPEP       82     82
SQ   SEQUENCE   82 AA;  9031 MW;  F4CEA5E7B8D53E59 CRC64;

  Query Match             65.4%;  Score 42.5;  DB 1;  Length 82;
  Best Local Similarity   58.3%;  Pred. No. 2;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         48 CDCCGERGECVC 59


RESULT 8
TX5A_PHONI
ID   TX5A_PHONI     STANDARD;      PRT;    82 AA.
AC   O76199;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Neurotoxin Pn2-5A precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99053403; PubMed=9839668;
RA   Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA   Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RT   "Cloning of cDNAS encoding neurotoxic peptides from the spider
RT   Phoneutria nigriventer.";
RL   Toxicon 36:1843-1850(1998).
CC   -!- FUNCTION: Blocks voltage-gated sodium channels (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF014463; AAC26165.1; -.
KW   Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     34       BY SIMILARITY.
FT   CHAIN        35     81       NEUROTOXIN PN2-5A.
FT   PROPEP       82     82       BY SIMILARITY.
SQ   SEQUENCE   82 AA;  8856 MW;  11DAF1EBE78B318F CRC64;

  Query Match             65.4%;  Score 42.5;  DB 1;  Length 82;
  Best Local Similarity   58.3%;  Pred. No. 2;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         48 CDCCGERGECVC 59


RESULT 9
TX21_PHONI
ID   TX21_PHONI     STANDARD;      PRT;    88 AA.
AC   P29423;
DT   01-APR-1993 (Rel. 25, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neurotoxin Tx2-1 precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99053403; PubMed=9839668;
RA   Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA   Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RT   "Cloning of cDNAS encoding neurotoxic peptides from the spider
RT   Phoneutria nigriventer.";
RL   Toxicon 36:1843-1850(1998).
RN   [2]
RP   SEQUENCE OF 35-87.
RC   TISSUE=Venom;
RX   MEDLINE=93011905; PubMed=1397265;
RA   Cordeiro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA   Gilroy J., Richardson M.;
RT   "The purification and amino acid sequences of four Tx2 neurotoxins
RT   from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT   (Keys).";
RL   FEBS Lett. 310:153-156(1992).
CC   -!- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,
CC       lacrimation, hypersalivation, sweating and agitation followed by
CC       spastic paralysis of the anterior and posterior extremities and
CC       death at dose levels of 1.62 mg/mouse. Insecticidal to the larval
CC       and adult forms of the house fly.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF014464; AAC26166.1; -.
KW   Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     34
FT   CHAIN        35     87       NEUROTOXIN TX2-1.
FT   PROPEP       88     88
SQ   SEQUENCE   88 AA;  9841 MW;  D8AD07C6A769E647 CRC64;

  Query Match             65.4%;  Score 42.5;  DB 1;  Length 88;
  Best Local Similarity   58.3%;  Pred. No. 2.2;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         48 CDCCGERGECVC 59


RESULT 10
TX1A_PHONI
ID   TX1A_PHONI     STANDARD;      PRT;   115 AA.
AC   O76198;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Neurotoxin Pn2-1A precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99053403; PubMed=9839668;
RA   Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA   Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RT   "Cloning of cDNAS encoding neurotoxic peptides from the spider
RT   Phoneutria nigriventer.";
RL   Toxicon 36:1843-1850(1998).
CC   -!- FUNCTION: Blocks voltage-gated sodium channels (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF014462; AAC26164.1; -.
KW   Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     61       BY SIMILARITY.
FT   CHAIN        62    114       NEUROTOXIN PN2-1A.
FT   PROPEP      115    115       BY SIMILARITY.
SQ   SEQUENCE   115 AA;  12858 MW;  B7D3321750F7BA50 CRC64;

  Query Match             65.4%;  Score 42.5;  DB 1;  Length 115;
  Best Local Similarity   58.3%;  Pred. No. 2.8;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 CDC---RGDCFC 9
              |||   ||:| |
Db         75 CDCCGERGECVC 86


RESULT 11
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CRS5_YEAST
ID   CRS5_YEAST     STANDARD;      PRT;    69 AA.
AC   P41902;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Metallothionein-like protein CRS5.
GN   CRS5 OR YOR031W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95014318; PubMed=7929222;
RA   Culotta V.C., Howard W.R., Liu X.F.;
RT   "CRS5 encodes a metallothionein-like protein in Saccharomyces
RT   cerevisiae.";
RL   J. Biol. Chem. 269:25295-25302(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / FY1679;
RA   de Haan M., Maarse A.C., Grivell L.A.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Critical role in copper (specific) homeostasis and
CC       detoxification. May protect by directly chelating and sequestering
CC       copper ions.
CC   -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 13.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L29056; AAA66061.1; -.
DR   EMBL; X87331; -; NOT_ANNOTATED_CDS.
DR   PIR; A55011; A55011.
DR   GermOnline; 143619; -.
DR   SGD; S0005557; CRS5.
DR   GO; GO:0005507; F:copper ion binding; IMP.
DR   GO; GO:0010038; P:response to metal ion; IMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   PRINTS; PR00438; GFCYSKNOT.
KW   Metal-binding; Metal-thiolate cluster; Copper.
SQ   SEQUENCE   69 AA;  7321 MW;  CEEF91203A813FF4 CRC64;

  Query Match             63.1%;  Score 41;  DB 1;  Length 69;
  Best Local Similarity   71.4%;  Pred. No. 2.9;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCRGDC 7
              ||| |:|
Db          6 CDCEGEC 12


RESULT 12
LML2_CAEEL
ID   LML2_CAEEL     STANDARD;      PRT;  3672 AA.
AC   Q21313;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Laminin-like protein K08C7.3 precursor.
GN   K08C7.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Berks M.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 1 laminin IV domain.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z70286; CAA94293.1; -.
DR   PIR; T23433; T23433.
DR   HSSP; P02468; 1KLO.
DR   WormPep; K08C7.3; CE06136.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR008211; LamNT.
DR   Pfam; PF00052; laminin_B; 1.
DR   Pfam; PF00053; laminin_EGF; 20.
DR   Pfam; PF00054; laminin_G; 5.
DR   Pfam; PF00055; laminin_Nterm; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00180; EGF_Lam; 17.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 4.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 21.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Hypothetical protein; Laminin EGF-like domain; Signal; Repeat.
FT   SIGNAL       1     27       POTENTIAL.
FT   CHAIN       28   3672       LAMININ-LIKE PROTEIN K08C7.3.
FT   DOMAIN      28    297       LAMININ N-TERMINAL (DOMAIN VI).
FT   DOMAIN     298    356       LAMININ EGF-LIKE 1.
FT   DOMAIN     357    426       LAMININ EGF-LIKE 2.
FT   DOMAIN     427    471       LAMININ EGF-LIKE 3.
FT   DOMAIN     472    518       LAMININ EGF-LIKE 4.
FT   DOMAIN     519    563       LAMININ EGF-LIKE 5.
FT   DOMAIN     564    609       LAMININ EGF-LIKE 6.
FT   DOMAIN     610    655       LAMININ EGF-LIKE 7.
FT   DOMAIN     656    700       LAMININ EGF-LIKE 8.
FT   DOMAIN     701    755       LAMININ EGF-LIKE 9.
FT   DOMAIN     756    808       LAMININ EGF-LIKE 10.
FT   DOMAIN     809    839       LAMININ EGF-LIKE 11 (INCOMPLETE).
FT   DOMAIN    1415   1460       LAMININ EGF-LIKE 12.
FT   DOMAIN    1461   1505       LAMININ EGF-LIKE 13.
FT   DOMAIN    1506   1553       LAMININ EGF-LIKE 14.
FT   DOMAIN    1554   1604       LAMININ EGF-LIKE 15.
FT   DOMAIN    1605   1614       LAMININ EGF-LIKE 16 (N-TERMINAL).
FT   DOMAIN    1615   1796       LAMININ DOMAIN IV.
FT   DOMAIN    1797   1829       LAMININ EGF-LIKE 16 (C-TERMINAL).
FT   DOMAIN    1830   1879       LAMININ EGF-LIKE 17.
FT   DOMAIN    1880   1936       LAMININ EGF-LIKE 18.
FT   DOMAIN    1937   1989       LAMININ EGF-LIKE 19.
FT   DOMAIN    1990   2036       LAMININ EGF-LIKE 20.
FT   DOMAIN    2037   2083       LAMININ EGF-LIKE 21.
FT   DOMAIN    2084   2131       LAMININ EGF-LIKE 22.
FT   DOMAIN    2693   2884       LAMININ G-LIKE 1.
FT   DOMAIN    2896   3066       LAMININ G-LIKE 2.
FT   DOMAIN    3072   3235       LAMININ G-LIKE 3.
FT   DOMAIN    3310   3482       LAMININ G-LIKE 4.
FT   DOMAIN    3488   3669       LAMININ G-LIKE 5.
FT   DISULFID   298    307       BY SIMILARITY.
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FT   DISULFID   300   320       BY SIMILARITY.
FT   DISULFID   322   331       BY SIMILARITY.
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FT   DISULFID   357   366       BY SIMILARITY.
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FT   DISULFID   493   502       BY SIMILARITY.
FT   DISULFID   505   516       BY SIMILARITY.
FT   DISULFID   519   531       BY SIMILARITY.
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FT   DISULFID   564   576       BY SIMILARITY.
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FT   DISULFID   610   622       BY SIMILARITY.
FT   DISULFID   612   629       BY SIMILARITY.
FT   DISULFID   631   640       BY SIMILARITY.
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FT   DISULFID   688   698       BY SIMILARITY.
FT   DISULFID   701   715       BY SIMILARITY.
FT   DISULFID   703   724       BY SIMILARITY.
FT   DISULFID   726   735       BY SIMILARITY.
FT   DISULFID   738   753       BY SIMILARITY.
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FT   DISULFID   779   788       BY SIMILARITY.
FT   DISULFID   791   806       BY SIMILARITY.
FT   DISULFID  1415  1427       BY SIMILARITY.
FT   DISULFID  1417  1434       BY SIMILARITY.
FT   DISULFID  1436  1445       BY SIMILARITY.
FT   DISULFID  1448  1458       BY SIMILARITY.
FT   DISULFID  1461  1469       BY SIMILARITY.
FT   DISULFID  1463  1476       BY SIMILARITY.
FT   DISULFID  1478  1487       BY SIMILARITY.
FT   DISULFID  1490  1503       BY SIMILARITY.
FT   DISULFID  1506  1520       BY SIMILARITY.
FT   DISULFID  1508  1527       BY SIMILARITY.
FT   DISULFID  1529  1538       BY SIMILARITY.
FT   DISULFID  1541  1551       BY SIMILARITY.
FT   DISULFID  1554  1566       BY SIMILARITY.
FT   DISULFID  1556  1573       BY SIMILARITY.
FT   DISULFID  1575  1584       BY SIMILARITY.
FT   DISULFID  1587  1602       BY SIMILARITY.
FT   DISULFID  1830  1839       BY SIMILARITY.
FT   DISULFID  1832  1846       BY SIMILARITY.
FT   DISULFID  1849  1858       BY SIMILARITY.
FT   DISULFID  1861  1877       BY SIMILARITY.
FT   DISULFID  1880  1894       BY SIMILARITY.
FT   DISULFID  1882  1905       BY SIMILARITY.
FT   DISULFID  1907  1916       BY SIMILARITY.
FT   DISULFID  1919  1934       BY SIMILARITY.
FT   DISULFID  1937  1951       BY SIMILARITY.
FT   DISULFID  1939  1958       BY SIMILARITY.
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FT   DISULFID  1992  2007       BY SIMILARITY.
FT   DISULFID  2009  2018       BY SIMILARITY.
FT   DISULFID  2021  2034       BY SIMILARITY.
FT   DISULFID  2037  2048       BY SIMILARITY.
FT   DISULFID  2039  2055       BY SIMILARITY.
FT   DISULFID  2057  2066       BY SIMILARITY.
FT   DISULFID  2069  2081       BY SIMILARITY.
FT   DISULFID  2084  2096       BY SIMILARITY.
FT   DISULFID  2086  2103       BY SIMILARITY.
FT   DISULFID  2105  2114       BY SIMILARITY.
FT   DISULFID  2117  2129       BY SIMILARITY.
FT   CARBOHYD   121   121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   140   140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   249   249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   351   351       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   477   477       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   511   511       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   530   530       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   634   634       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   761   761       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1014  1014       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1341  1341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1705  1705       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1756  1756       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1868  1868       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1944  1944       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1986  1986       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2002  2002       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2159  2159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2207  2207       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2231  2231       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2235  2235       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2401  2401       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2421  2421       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2487  2487       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  2821  2821       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  3087  3087       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  3242  3242       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  3541  3541       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE  3672 AA;  404223 MW;  28E262DB5FF14BFA CRC64;

  Query Match           63.1%;  Score 41;  DB 1;  Length 3672;
  Best Local Similarity  55.6%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              ||  | |:|
Db        668 CDSNGQCYC 676


RESULT 13
ITBN_DROME
ID   ITBN_DROME     STANDARD;      PRT;   799 AA.
AC   Q27591; Q9VIG7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Integrin beta-nu precursor.
GN   BETA-INT-NU OR CG1762.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Midgut endoderm;
RX   MEDLINE=94357079; PubMed=8076521;
RA   Yee G.H., Hynes R.O.;
RT   "A novel, tissue-specific integrin subunit, beta nu, expressed in the
RT   midgut of Drosophila melanogaster.";
RL   Development 118:845-858(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- FUNCTION: PROBABLY PLAYS A ROLE IN CELL ADHESION.
CC   -!- SUBUNIT: Heterodimer of an alpha and a beta subunit.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the integrin beta chain family.
CC   -!- SIMILARITY: Contains 1 VWFA domain.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L13305; AAC37169.1; -.
DR   EMBL; AE003669; AAF53952.1; -.
DR   HSSP; P05106; 1JV2.
DR   FlyBase; FBgn0010395; beta-Int-nu.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   InterPro; IPR001169; Integrin_beta_C.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF00362; integrin_B; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   PRINTS; PR01186; INTEGRINB.
DR   ProDom; PD001811; Integrin_B; 1.
DR   SMART; SM00187; INB; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_4.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_4.
DR   PROSITE; PS00243; INTEGRIN_BETA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW   Signal.
FT   SIGNAL       1    26       POTENTIAL.
FT   CHAIN       27   799       INTEGRIN BETA-NU.
FT   DOMAIN      27   725       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   726   746       POTENTIAL.
FT   DOMAIN     747   799       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     136   372       VWFA.
FT   CARBOHYD    73    73       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   167   167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   409   409       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   505   505       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   655   655       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   680   680       E -> G (IN REF. 1).
FT   CONFLICT   701   701       V -> A (IN REF. 1).
SQ   SEQUENCE   799 AA;  90841 MW;  351869D523F07DEB CRC64;

  Query Match             62.3%;  Score 40.5;  DB 1;  Length 799;
  Best Local Similarity   38.9%;  Pred. No. 35;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    9;  Gaps    1;

Qy          1 CDCR---------GDCFC 9
              |:||           ||||
Db        552 CECRECLDCDEKLADCFC 569


RESULT 14
TASM_POVMA
ID   TASM_POVMA     STANDARD;      PRT;   195 AA.
AC   P03078;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Small T antigen.
OS   Mouse polyomavirus (strain A2), and
OS   Mouse polyomavirus (strain 3).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10636, 10635;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A2;
RX   MEDLINE=80099647; PubMed=6243401;
RA   Soeda E., Arrand J.R., Smolar N., Walsh J.E., Griffin B.E.;
RT   "Coding potential and regulatory signals of the polyoma virus
RT   genome.";
RL   Nature 283:445-453(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3;
RX   MEDLINE=80001963; PubMed=225042;
RA   Friedmann T., Esty A., Laporte P., Deininger P.L.;
RT   "The nucleotide sequence and genome organization of the polyoma early
RT   region: extensive nucleotide and amino acid homology with SV40.";
RL   Cell 17:715-724(1979).
CC   -!- SIMILARITY: Contains 1 J domain.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J02289; AAA46874.1; -.
DR   EMBL; J02288; AAB59899.1; -.
DR   PIR; C03635; TVVPA.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR003354; Papo_T_antigen.
DR   Pfam; PF00226; DnaJ; 1.
DR   Pfam; PF02380; Papo_T_antigen; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR   PROSITE; PS50076; DNAJ_2; FALSE_NEG.
KW   Early protein.
```

```
FT   DOMAIN       12     75       J-DOMAIN.
SQ   SEQUENCE   195 AA;  22811 MW;  44EED6711E1AFEC3 CRC64;

  Query Match             61.5%;  Score 40;  DB 1;  Length 195;
  Best Local Similarity   53.8%;  Pred. No. 11;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 CDCR----GDCFC 9
              || |    |:|||
Db        138 CDARCLVLGECFC 150


RESULT 15
TAMI_POVMA
ID   TAMI_POVMA     STANDARD;      PRT;   421 AA.
AC   P03077;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Middle T antigen.
OS   Mouse polyomavirus (strain A2).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10636;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80099647; PubMed=6243401;
RA   Soeda E., Arrand J.R., Smolar N., Walsh J.E., Griffin B.E.;
RT   "Coding potential and regulatory signals of the polyoma virus
RT   genome.";
RL   Nature 283:445-453(1980).
CC   -!- SIMILARITY: Contains 1 J domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J02288; AAB59900.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR003354; Papo_T_antigen.
DR   Pfam; PF00226; DnaJ; 1.
DR   Pfam; PF02380; Papo_T_antigen; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR   PROSITE; PS50076; DNAJ_2; FALSE_NEG.
KW   Early protein.
FT   DOMAIN       12     75       J-DOMAIN.
SQ   SEQUENCE   421 AA;  48622 MW;  CA0C25C4984CACB7 CRC64;

  Query Match             61.5%;  Score 40;  DB 1;  Length 421;
  Best Local Similarity   53.8%;  Pred. No. 23;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 CDCR----GDCFC 9
              || |    |:|||
Db        138 CDARCLVLGECFC 150


Search completed: July 11, 2004, 09:16:28
Job time : 12 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 39 Seconds
(without alignments)
72.812 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	69.2	676	10	Q8S1X3	Q8s1x3 oryza sativ
2	45	69.2	696	10	Q8L821	Q8l821 zea mays (m
3	44	67.7	114	11	Q9R151	Q9r151 cavia porce
4	44	67.7	439	16	Q87QB5	Q87qb5 vibrio para
5	44	67.7	787	6	Q863C4	Q863c4 ovis aries
6	44	67.7	788	6	Q8SQB8	Q8sqb8 bos taurus
7	43	66.2	954	5	Q9GYG8	Q9gyg8 caenorhabdi
8	42	64.6	463	10	Q9C599	Q9c599 arabidopsis
9	41	63.1	74	5	Q8WQ95	Q8wq95 crassostrea
10	41	63.1	218	10	Q851N3	Q851n3 oryza sativ
11	41	63.1	458	17	Q9HPQ4	Q9hpq4 halobacteri
12	41	63.1	535	4	Q96EB1	Q96eb1 homo sapien
13	41	63.1	546	12	Q80IB8	Q80ib8 influenza a
14	41	63.1	549	12	Q80IA8	Q80ia8 influenza a
15	41	63.1	552	12	Q80IC9	Q80ic9 influenza a
16	41	63.1	552	12	Q80IC5	Q80ic5 influenza a
17	41	63.1	552	12	Q80IB9	Q80ib9 influenza a
18	41	63.1	552	12	Q80IB7	Q80ib7 influenza a
19	41	63.1	552	12	Q80IA1	Q80ia1 influenza a
20	41	63.1	552	12	Q80I97	Q80i97 influenza a
21	41	63.1	552	12	Q80I95	Q80i95 influenza a
22	41	63.1	552	12	Q80I82	Q80i82 influenza a
23	41	63.1	736	10	Q9SVX7	Q9svx7 arabidopsis
24	41	63.1	1162	5	Q8WTP0	Q8wtp0 halocynthia
25	41	63.1	3704	5	P91904	P91904 caenorhabdi
26	40	61.5	100	5	Q962G0	Q962g0 littorina l
27	40	61.5	116	12	Q9IBN0	Q9ibn0 polyomaviru
28	40	61.5	119	12	Q84251	Q84251 polyomaviru
29	40	61.5	167	12	Q84326	Q84326 polyomaviru
30	40	61.5	195	11	Q04190	Q04190 mus musculu
31	40	61.5	196	12	Q8V9F4	Q8v9f4 murine poly
32	40	61.5	211	12	Q84854	Q84854 polyomaviru
33	40	61.5	214	12	Q84252	Q84252 polyomaviru
34	40	61.5	313	5	Q24330	Q24330 dictyosteli
35	40	61.5	320	5	Q7Z1Y7	Q7z1y7 loxosceles
36	40	61.5	365	16	Q81QZ7	Q81qz7 bacillus an
37	40	61.5	421	11	Q04188	Q04188 mus musculu
38	40	61.5	421	12	Q89765	Q89765 murine poly
39	40	61.5	494	11	Q9QZE6	Q9qze6 mus musculu
40	40	61.5	625	10	Q9LP82	Q9lp82 arabidopsis
41	40	61.5	677	13	Q7SZW3	Q7szw3 brachydanio
42	40	61.5	690	13	Q7ZYY6	Q7zyy6 brachydanio
43	40	61.5	711	13	Q7ZYY8	Q7zyy8 brachydanio
44	40	61.5	729	13	Q7SZW2	Q7szw2 brachydanio
45	40	61.5	768	13	Q98TH8	Q98th8 cyprinus ca

ALIGNMENTS

RESULT 1
Q8S1X3
ID Q8S1X3 PRELIMINARY; PRT; 676 AA.
AC Q8S1X3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative SUVH4.
GN P0482D04.21 OR OSJNBA0093F16.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0482D04.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNBa0093F16.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003262; BAB89674.1; -.
DR EMBL; AP004332; BAB92897.1; -.
DR Gramene; Q8S1X3; -.
DR InterPro; IPR003105; G9a.
DR InterPro; IPR003616; PostSET.
DR InterPro; IPR007728; Pre-SET.
DR InterPro; IPR001214; SET.
DR Pfam; PF05033; Pre-SET; 1.
DR Pfam; PF00856; SET; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR PROSITE; PS50868; POST_SET; 1.

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DR   PROSITE; PS50867; PRE_SET; 1.
DR   PROSITE; PS50280; SET; 1.
SQ   SEQUENCE   676 AA;  74816 MW;  92677BDC449DCF68 CRC64;

  Query Match             69.2%;  Score 45;  DB 10;  Length 676;
  Best Local Similarity   85.7%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCRGDC 7
              ||| |||
Db        435 CDCEGDC 441


RESULT 2
Q8L821
ID   Q8L821      PRELIMINARY;      PRT;   696 AA.
AC   Q8L821;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   SET domain-containing protein SET118.
GN   SET118.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. B73;
RA   Chandler V.L., Kaeppler S.M., Kaeppler H.F., Cone K.C.;
RT   "Sequences from the Plant Chromatin Consortium (NSF Plant Genome
RT   Program Grant 9975930).";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. B73;
RA   Bergstrom D.E., Springer N.M., Schmitt L.T., Guthrie E., Sidorenko L.,
RA   Selinger D., Kaeppler S.M., Cone K.C.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
DR   EMBL; AY122271; AAM89287.1; -.
DR   InterPro; IPR003105; G9a.
DR   InterPro; IPR003616; PostSET.
DR   InterPro; IPR007728; Pre-SET.
DR   InterPro; IPR001214; SET.
DR   InterPro; IPR003606; Zn2-binding.
DR   Pfam; PF05033; Pre-SET; 1.
DR   Pfam; PF00856; SET; 1.
DR   Pfam; PF02182; YDG_SRA; 1.
DR   SMART; SM00508; PostSET; 1.
DR   SMART; SM00468; PreSET; 1.
DR   SMART; SM00317; SET; 1.
DR   SMART; SM00466; SRA; 1.
DR   PROSITE; PS50868; POST_SET; 1.
DR   PROSITE; PS50867; PRE_SET; 1.
DR   PROSITE; PS50280; SET; 1.
SQ   SEQUENCE   696 AA;  76861 MW;  6F30A9018126C9AD CRC64;

  Query Match             69.2%;  Score 45;  DB 10;  Length 696;
  Best Local Similarity   85.7%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCRGDC 7
              ||| |||
Db        455 CDCEGDC 461


RESULT 3
Q9R151
ID   Q9R151      PRELIMINARY;      PRT;   114 AA.
AC   Q9R151;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Integrin beta 6 (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Trachea;
RA   Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA   Sekizawa K.;
RT   "Guinea-pig beta-6 integrin expression in injured tracheal
RT   epithelium.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF169344; AAD49344.1; -.
DR   HSSP; P05106; 1JV2.
DR   GO; GO:0008305; C:integrin complex; IEA.
DR   GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR   GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   Pfam; PF00362; integrin_B; 1.
DR   ProDom; PD001811; Integrin_B; 1.
DR   PROSITE; PS00022; EGF_1; 1.
FT   NON_TER       1       1
FT   NON_TER     114     114
SQ   SEQUENCE   114 AA;  12121 MW;  95D4528EBD0435EF CRC64;

  Query Match             67.7%;  Score 44;  DB 11;  Length 114;
  Best Local Similarity   66.7%;  Pred. No. 4.3;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        104 CSGRGDCYC 112


RESULT 4
Q87QB5
ID   Q87QB5      PRELIMINARY;      PRT;   439 AA.
AC   Q87QB5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Iron-containing alcohol dehydrogenase.
GN   VP1235.
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
DR   EMBL; AP005077; BAC59498.1; -.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR001670; Fe-ADH.
DR   Pfam; PF00465; Fe-ADH; 1.
KW   Complete proteome.
SQ   SEQUENCE   439 AA;  47354 MW;  BA1A035739CF1953 CRC64;

  Query Match             67.7%;  Score 44;  DB 16;  Length 439;
  Best Local Similarity   85.7%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 CDCRGDC 7
              ||| |||
Db        408 CDCSGDC 414


RESULT 5
Q863C4
ID   Q863C4      PRELIMINARY;      PRT;   787 AA.
AC   Q863C4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Integrin subunit beta-6 (Fragment).
GN   ITB6.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Upper airway;
RA   McAleese S.M., Collie D.D.S., Miller H.R.P.;
RT   "Cloning and sequencing of the cDNA for sheep integrin subunit beta-
RT   6.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ439062; CAD27749.1; -.
DR   GO; GO:0008305; C:integrin complex; IEA.
DR   GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR   GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR   GO; GO:0007275; P:development; IEA.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   InterPro; IPR001169; Integrin_beta_C.
DR   InterPro; IPR003659; Plexin-like.
DR   Pfam; PF00362; integrin_B; 1.
DR   PRINTS; PR01186; INTEGRINB.
DR   ProDom; PD001811; Integrin_B; 1.
DR   SMART; SM00187; INB; 1.
DR   SMART; SM00423; PSI; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00243; INTEGRIN_BETA; 2.
KW   Integrin.
FT   NON_TER       1      1
SQ   SEQUENCE   787 AA;  85745 MW;  B7AC4903A9C7A89E CRC64;

  Query Match             67.7%;  Score 44;  DB 6;  Length 787;
  Best Local Similarity   66.7%;  Pred. No. 21;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        511 CSGRGDCYC 519


RESULT 6
Q8SQB8
ID   Q8SQB8      PRELIMINARY;      PRT;   788 AA.
AC   Q8SQB8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Integrin beta 6 subunit precursor protein.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Duque H., Baxt B.;
RT   "Foot-and-mouth disease virus receptors: comparison of bovine alpha V
RT   integrin utilization by lab- and field-strain viruses.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
CC       BONDS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
DR   EMBL; AF468060; AAL78039.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008305; C:integrin complex; IEA.
DR   GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR   GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR   GO; GO:0007275; P:development; IEA.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002369; Integrin_B.
DR   InterPro; IPR001169; Integrin_beta_C.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF00362; integrin_B; 1.
DR   PRINTS; PR01186; INTEGRINB.
DR   ProDom; PD001811; Integrin_B; 1.
DR   SMART; SM00187; INB; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00243; INTEGRIN_BETA; 2.
KW   Cell adhesion; Glycoprotein; Integrin; Repeat; Signal; Transmembrane.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    788       INTEGRIN BETA 6 SUBUNIT.
SQ   SEQUENCE   788 AA;  85892 MW;  FB9B5197BFF56EEB CRC64;

  Query Match             67.7%;  Score 44;  DB 6;  Length 788;
  Best Local Similarity   66.7%;  Pred. No. 21;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |  ||||:|
Db        511 CSGRGDCYC 519


RESULT 7
Q9GYG8
ID   Q9GYG8      PRELIMINARY;      PRT;   954 AA.
AC   Q9GYG8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   W01C8.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Nhan M.;
RT   "The sequence of C. elegans cosmid W01C8.";
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
```

```
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
DR   EMBL; U41508; AAG00027.2; -.
DR   WormPep; W01C8.3; CE30196.
DR   InterPro; IPR001214; SET.
DR   Pfam; PF00856; SET; 1.
DR   SMART; SM00317; SET; 1.
DR   PROSITE; PS50280; SET; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   954 AA;  107835 MW;  E7747E40ADD941B5 CRC64;

  Query Match             66.2%;  Score 43;  DB 5;  Length 954;
  Best Local Similarity   85.7%;  Pred. No. 36;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCRGDC 7
              | |||||
Db        144 CGCRGDC 150


RESULT 8
Q9C599
ID   Q9C599      PRELIMINARY;      PRT;   463 AA.
AC   Q9C599;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   AT5G08780.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA   Rudd S., Lemcke K., Mayer K.F.X.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL590346; CAC35883.1; -.
DR   HSSP; P02259; 1HST.
DR   GO; GO:0000786; C:nucleosome; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
DR   GO; GO:0006334; P:nucleosome assembly; IEA.
DR   InterPro; IPR005818; Histone_H1/H5.
DR   InterPro; IPR003216; Linkerhist_N.
DR   Pfam; PF00538; linker_histone; 1.
DR   ProDom; PD000373; Linkerhist_N; 1.
DR   SMART; SM00526; H15; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   463 AA;  52015 MW;  781A08F0BB11DCAA CRC64;

  Query Match             64.6%;  Score 42;  DB 10;  Length 463;
  Best Local Similarity   62.5%;  Pred. No. 29;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCF 8
              |||  ||:
Db        114 CDCNNDCY 121


RESULT 9
Q8WQ95
ID   Q8WQ95      PRELIMINARY;      PRT;    74 AA.
AC   Q8WQ95;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Metallothionein (Fragment).
GN   MT3.
OS   Crassostrea gigas (Pacific oyster).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
OC   Ostreoidea; Ostreidae; Crassostrea.
OX   NCBI_TaxID=29159;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Gill;
RA   Tanguy A., Boutet I., Moraga D.;
RT   "Cloning and characterization of a third metallothionein gene in the
RT   Pacific oyster Crassostrea gigas: a singular case.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ295157; CAC82788.1; -.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   InterPro; IPR003019; Metallthion_.
DR   InterPro; IPR001008; Metallthion_2.
DR   Pfam; PF00131; metalthio; 1.
DR   PRINTS; PR00875; MTMOLLUSC.
FT   NON_TER       1      1
SQ   SEQUENCE   74 AA;  7274 MW;  5D9DD049577B74AE CRC64;

  Query Match             63.1%;  Score 41;  DB 5;  Length 74;
  Best Local Similarity   55.6%;  Pred. No. 9.3;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |:| | | |
Db         46 CNCNGSCAC 54


RESULT 10
Q851N3
ID   Q851N3      PRELIMINARY;      PRT;   218 AA.
AC   Q851N3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OSJNBA0042I09.11.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0042I09 genomic sequence.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC104487; AAO41141.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   218 AA;  24562 MW;  4FE0A501A4A17507 CRC64;

  Query Match             63.1%;  Score 41;  DB 10;  Length 218;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 DCRGDC 7
              ||||||
Db        202 DCRGDC 207


RESULT 11
```

```
Q9HPQ4
ID   Q9HPQ4      PRELIMINARY;      PRT;   458 AA.
AC   Q9HPQ4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vng1524c.
GN   VNG1524C.
OS   Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC   Halobacteriaceae; Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR   EMBL; AE005065; AAG19813.1; -.
DR   PIR; A84306; A84306.
DR   GO; GO:0008483; F:transaminase activity; IEA.
DR   InterPro; IPR005814; Aminotrans_3.
DR   InterPro; IPR001220; Lectin_legB.
DR   Pfam; PF00202; aminotran_3; 1.
DR   PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
DR   PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
KW   Complete proteome.
SQ   SEQUENCE   458 AA;  49439 MW;  B1EA7132978E0F0E CRC64;

  Query Match             63.1%;  Score 41;  DB 17;  Length 458;
  Best Local Similarity   55.6%;  Pred. No. 42;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              | | |:| |
Db        198 CTCEGECSC 206


RESULT 12
Q96EB1
ID   Q96EB1      PRELIMINARY;      PRT;   535 AA.
AC   Q96EB1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis, and Embryonic carcinoma;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012514; AAH12514.1; -.
DR   Genew; HGNC:1171; ELP4.
DR   InterPro; IPR008728; PAXNEB.
DR   Pfam; PF05625; PAXNEB; 1.
SQ   SEQUENCE   535 AA;  58713 MW;  86E6DD3B545E96D4 CRC64;

  Query Match             63.1%;  Score 41;  DB 4;  Length 535;
  Best Local Similarity   71.4%;  Pred. No. 47;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CRGDCFC 9
                |:||| |
Db        522 CKGDCIC 528


RESULT 13
Q80IB8
ID   Q80IB8      PRELIMINARY;      PRT;   546 AA.
AC   Q80IB8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hemagglutinin (Fragment).
OS   Influenza A virus (A/chicken/NJ/9777-7/98(H7N2)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=226628;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/Chicken/NJ/9777-7/98;
RA   Spackman E., Suarez D.L., Senne D.A., Davison S.;
RT   "Sequence Anylisis of Recent H7 Avian Influenza Viruses Associated
RT   with Three Different Outbreaks in Commercial Poultry in the US.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY240889; AAO86916.1; -.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   546 AA;  60823 MW;  016872FCF44D2197 CRC64;

  Query Match             63.1%;  Score 41;  DB 12;  Length 546;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CRGDCF 8
              ||||||
Db        272 CRGDCF 277


RESULT 14
Q80IA8
ID   Q80IA8      PRELIMINARY;      PRT;   549 AA.
AC   Q80IA8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hemagglutinin (Fragment).
OS   Influenza A virus (A/chicken/PA/143586/01(H7N2)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=226638;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/Chicken/PA/143586/01;
RA   Spackman E., Suarez D.L., Senne D.A., Davison S.;
RT   "Sequence Anylisis of Recent H7 Avian Influenza Viruses Associated
RT   with Three Different Outbreaks in Commercial Poultry in the US.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY240899; AAO86926.1; -.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   549 AA;  61013 MW;  3E9D2F2327E0D8F9 CRC64;

  Query Match             63.1%;  Score 41;  DB 12;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 CRGDCF 8
              ||||||
Db        275 CRGDCF 280


RESULT 15
Q80IC9
ID   Q80IC9      PRELIMINARY;      PRT;   552 AA.
AC   Q80IC9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hemagglutinin.
OS   Influenza A virus (A/avian/NY/70411-12/00(H7N2)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses; Influenzavirus A.
OX   NCBI_TaxID=226617;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/Avian/NY/70411-12/00;
RA   Spackman E., Suarez D.L., Senne D.A., Davison S.;
RT   "Sequence Anylisis of Recent H7 Avian Influenza Viruses Associated
RT   with Three Different Outbreaks in Commercial Poultry in the US.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY240878; AAO86905.1; -.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
SQ   SEQUENCE   552 AA;  61407 MW;  C80AD822D34B5C54 CRC64;

  Query Match             63.1%;  Score 41;  DB 12;  Length 552;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CRGDCF 8
              ||||||
Db        278 CRGDCF 283


Search completed: July 11, 2004, 09:14:58
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 55 Seconds
(without alignments)
46.235 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	9	2	AAR76200	Aar76200 Alphav/be
2	65	100.0	9	2	AAW60289	Aaw60289 Tumour ho
3	65	100.0	9	2	AAW56034	Aaw56034 Chimeric
4	65	100.0	9	2	AAY42255	Aay42255 Synthetic
5	65	100.0	9	2	AAY43233	Aay43233 RGD-conta
6	65	100.0	9	2	AAW93626	Aaw93626 NGR recep
7	65	100.0	9	2	AAY48821	Aay48821 Membrane
8	65	100.0	9	3	AAY54271	Aay54271 Alpha Vbe
9	65	100.0	9	3	AAY44970	Aay44970 RGD-4C ta
10	65	100.0	9	3	AAB17928	Aab17928 TPO-mimet
11	65	100.0	9	3	AAB17964	Aab17964 Integrin-
12	65	100.0	9	3	AAB17346	Aab17346 Integrin-
13	65	100.0	9	3	AAY90211	Aay90211 Alphav in
14	65	100.0	9	3	AAO22875	Aao22875 Angiogeni
15	65	100.0	9	3	AAB21701	Aab21701 Human bre
16	65	100.0	9	4	AAB20271	Aab20271 Peptide t
17	65	100.0	9	4	AAB50242	Aab50242 Enhanced
18	65	100.0	9	4	AAB97086	Aab97086 Integrin-
19	65	100.0	9	4	AAE06279	Aae06279 Tumour ho
20	65	100.0	9	4	AAE11044	Aae11044 RGD-conta
21	65	100.0	9	5	AAU98837	Aau98837 Tumour ho
22	65	100.0	9	5	ABG35079	Abg35079 RGD-4C-be
23	65	100.0	9	5	AAU81110	Aau81110 Integrin-
24	65	100.0	9	5	AAU81134	Aau81134 Integrin-
25	65	100.0	9	5	ABP54051	Abp54051 Alpha-v-b
26	65	100.0	9	5	ABB72945	Abb72945 Integrin
27	65	100.0	9	5	ABB72961	Abb72961 Integrin
28	65	100.0	9	5	ABJ04359	Abj04359 BRASIL me
29	65	100.0	9	5	ABB08066	Abb08066 Cyclic RG
30	65	100.0	9	5	ABG70729	Abg70729 avB3 bind
31	65	100.0	9	5	ABB76442	Abb76442 RGD-4C Pe
32	65	100.0	9	5	AAE17983	Aae17983 Human lig
33	65	100.0	9	5	ABB78354	Abb78354 Aminc aci
34	65	100.0	9	5	ABG70754	Abg70754 Targeting
35	65	100.0	9	5	AAU75609	Aau75609 Synthetic
36	65	100.0	9	5	AAU79138	Aau79138 Synthetic
37	65	100.0	9	5	AAU98972	Aau98972 Adeno-ass
38	65	100.0	9	5	AAM48795	Aam48795 Tumour-ta
39	65	100.0	9	5	ABB79525	Abb79525 RGD motif
40	65	100.0	9	5	ABG31063	Abg31063 Alpha v b
41	65	100.0	9	5	AAG78427	Aag78427 Cyclic pe
42	65	100.0	9	5	AAM51995	Aam51995 Drug targ
43	65	100.0	9	6	ABG73024	Abg73024 Integrin
44	65	100.0	9	6	ABB84641	Abb84641 Human int
45	65	100.0	9	6	ABU59556	Abu59556 Tumour an

ALIGNMENTS

RESULT 1
AAR76200
ID AAR76200 standard; peptide; 9 AA.
XX
AC AAR76200;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alphav/beta3 and alphav/beta5 integrin binding peptide #4.
XX
KW High affinity; integrin binding peptide; alpha5/beta1; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachemnt; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
PN WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US013542.
XX
PR 24-NOV-1993; 93US-00158001.
PR 04-AUG-1994; 94US-00286861.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Ruoslahti E, Koivunen E;
XX
DR WPI; 1995-206899/27.
XX
PT High affinity integrin binding peptides - can be used to attach cells to
PT a substrate, inhibit the attachment of osteoclasts to bone, promote wound
PT healing, inhibit angiogenesis, metastasis of tumours and migration of
PT smooth muscle cells.
XX
PS Claim 21; Page 62; 86pp; English.
XX
CC The sequences given in AAR76185-200 and AAR79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides which
CC bind to alpha5/beta1 integrins contain the motifs given in AAR76185-86
CC and peptides which bind to alphav/beta5 and alphav/beta3 integrins
CC contain the motif given in AAR76187. Alphav/beta5 integrins are also
CC bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the formation
CC of a disulphide bond, a peptide bond or a lactam bond. These peptides may
CC be used for isolating the complementary integrin from a sample mixture by

CC contacting them under ionic conditions to allow binding of the integrin
CC to the peptide and then separating the integrin from the peptide. They
CC can be used for attaching cells to a substrate, by binding them to the
CC substrate with the cell. The peptides promote wound healing when applied
CC locally and inhibit the attachment of osteoclasts to bone. They inhibit
CC angiogenesis, metastasis of tumours and migration of smooth muscle cells
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 2
AAW60289
ID AAW60289 standard; peptide; 9 AA.
XX
AC AAW60289;
XX
DT 24-AUG-1998 (first entry)
XX
DE Tumour homing peptide of the invention.
XX
KW Tumour homing peptide; in vivo panning;
KW alpha-V-containing integrin binding motif; tumour.
XX
OS Unidentified.
XX
PN WO9810795-A2.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US016086.
XX
PR 10-SEP-1996; 96US-00710067.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti E, Pasqualini R;
XX
DR WPI; 1998-207151/18.
XX
PT Tumour homing molecules and their conjugates - useful for, e g. directing
PT linked moiety to tumour containing angiogenic vasculature.
XX
PS Claim 6; Page 91; 105pp; English.
XX
CC The present peptide represents a tumour homing peptide, and is produced
CC by in vivo panning. The peptide has an alpha-V-containing integrin
CC binding motif, Arg-Gly-Asp (RGD). The in vivo panning comprises
CC administering a library of diverse peptides to a subject having a tumour,
CC collecting a sample of the tumour, identifying a peptide that homes to
CC the tumour, collecting a sample of normal tissue corresponding to the
CC tumour, and determining that the peptide that homes to the tumour is not
CC present in the normal tissue. The tumour homing peptide can be linked to
CC a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 3
AAW56034
ID AAW56034 standard; peptide; 9 AA.
XX
AC AAW56034;
XX
DT 29-JUL-1998 (first entry)
XX
DE Chimeric adenovirus fiber protein non-native amino acid sequence 3.
XX
KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.
XX
OS Synthetic.
OS Mastadenovirus.
XX
PN WO9807865-A1.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997; 97WO-US014719.
XX
PR 21-AUG-1996; 96US-00701124.
XX
PA (GENV-) GENVEC INC.
XX
PI Wickham TJ, Roelvink PW, Kovesdi I;
XX
DR WPI; 1998-169169/15.
XX
PT Chimeric adenovirus fibre proteins - containing non-native amino acid
PT sequence to provide for binding and entry into cells, especially for gene
PT therapy.
XX
PS Claim 7; Page 68; 124pp; English.
XX
CC The present sequence represents a specifically claimed non-native amino
CC acid sequence from a chimeric adenovirus fibre protein (AFP) of the
CC present invention. The non-native amino acid sequence allows the chimeric
CC fibre (or a vector comprising the chimeric fibre) to more efficiently
CC bind to and enter cells. The products can be used for gene therapy, for
CC treating cancer, e.g. melanoma, glioma and lung cancers as well as
CC genetic disorders, e.g. cystic fibrosis, haemophilia and muscular
CC dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and
CC hepatitis and also for heart disease, to e.g. prevent restenosis
CC following angioplasty or to promote angiogenesis to reperfuse necrotic
CC tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,
CC rheumatoid arthritis, and Alzheimer's disease
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 4
AAY42255
ID AAY42255 standard; peptide; 9 AA.
XX
AC AAY42255;
XX
DT 01-DEC-1999 (first entry)
XX
DE Synthetic RGD-4C peptide.
XX
KW Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;
KW cancer; cystic fibrosis; muscular dystrophy.

XX
OS Synthetic.
XX
PN WO9939734-A1.
XX
PD 12-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US002549.
XX
PR 06-FEB-1998; 98US-0073947P.
PR 10-SEP-1998; 98US-0099801P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Curiel DT, Krasnykh VN, Dmitriev I;
XX
DR WPI; 1999-539951/45.
XX
PT Recombinant adenovirus vectors with modified fiber knob loops, useful in
PT gene therapy.
XX
PS Example 21; Page 49; 126pp; English.
XX
CC This sequence represents a synthetic RGD-4C peptide. DNA encoding this
CC sequence was cloned into the sequence encoding the HI loop of the
CC adenovirus fibre protein knob domain. This was then used in the
CC construction of plasmids encoding a modified fibre protein. Recombinant
CC adenovirus genomes were generated by homologous DNA recombination in E.
CC coli, before excision of the newly generated genome for virus rescue. The
CC knob domain of the adenovirus fibre protein mediates the initial binding
CC and recognition of the coxsackievirus and adenovirus receptor (CAR) on
CC the cell surface. The HI loop protrudes from the knob domain and connects
CC beta-strands involved in the formation of the cell binding site.
CC Recombinant adenovirus vectors are used in a number of gene therapy
CC applications; however, the reliance on the CAR means that in certain
CC situations, recombinant virions are sequestered by high CAR-expressing
CC non-target cells while the true target cells, if low in CAR, receive
CC little of the therapeutic gene. Modification of the HI loop by
CC replacement of the hypervariable region of the loop with a peptide such
CC as the RGD peptide results in the ability of the virus to utilise an
CC alternative receptor during the cell entry process. Modifying the
CC adenovirus fibre knob protein in this way increases the ability of an
CC adenovirus to transduce a tumour cell in vitro, in vivo and ex vivo. The
CC vector Ad5FHIFLAG incorporating an RGD peptide demonstrated two to three
CC orders of magnitude of increased gene transfer to ovarian cancer cells.
CC The modified adenovirus has an altered tropism, which allows the
CC adenovirus to be targeted to selected cell types. The recombinant
CC adenovirus can be used to provide gene therapy for individuals suffering
CC from cancer, cystic fibrosis and Duchenne's muscular dystrophy
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 5
AAY43233
ID AAY43233 standard; peptide; 9 AA.
XX
AC AAY43233;
XX
DT 13-JAN-2000 (first entry)
XX
DE RGD-containing peptide #12.
XX
KW Nucleic acid delivery vehicle; bifunctional complex; transgene; CFTR;
KW cell surface targeting; cell surface molecule binding region; integrin;
KW cystic fibrosis transmembrane regulator; alpha1-antitrypsin;
KW suicide gene; beta-glucocerebrosidase; cell transfection; cell infection;
KW RGD peptide.
XX
OS Synthetic.
XX
PN WO9940214-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US002680.
XX
PR 09-FEB-1998; 98US-00020483.
PR 09-FEB-1998; 98US-0135092P.
PR 06-NOV-1998; 98US-0107471P.
XX
PA (GENZ) GENZYME CORP.
XX
PI O'riordan C, Romanczuk H, Wadsworth SC;
XX
DR WPI; 1999-610583/52.
XX
PT Nucleic acid delivery vehicles useful for transfecting and infecting a
PT target cell.
XX
PS Claim 22; Page 39; 118pp; English.
XX
CC This sequence represents a RGD-containing peptide that can be used in a
CC bifunctional complex used in the nucleic acid delivery vehicle (I) of the
CC invention. (I) is for transfecting and/or infecting a target cell, and
CC comprises a transgene and a bifunctional complex (B) that targets the
CC nucleic acid delivery vehicle to the cell surface. (B) comprises a
CC delivery vehicle binding portion, a cell surface molecule binding portion
CC (such as this sequence) and a linker connecting them. The delivery
CC vehicle can be specifically targeted to the cell via the binding to cell
CC surface molecules. (I) can be used to target cells, which express
CC integrins such as, HT-29 colon carcinoma cells, lymphocytes and
CC monocytes, blood platelets, SMC-90 human lung fibroblast, MG(63)
CC osteosarcoma cell line, vascular endothelial cells and melanoma cells.
CC (I) is useful for delivery of nucleic acids encoding CFTR (cystic
CC fibrosis transmembrane regulator), alpha1-antitrypsin, beta-
CC glucocerebrosidase and suicide genes. The construct increases the
CC efficiency of cellular uptake of (I). The constructs also enable the
CC transfection/infection of cells that are normally refractory to
CC transfection/infection by targeting cell receptors that are present on
CC such cells
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 6
AAW93626
ID AAW93626 standard; protein; 9 AA.
XX
AC AAW93626;
XX
DT 28-JUN-1999 (first entry)
XX
DE NGR receptor binding tumour homing peptide 5.
XX
KW Tumour homing peptide; tumour; diagnosis; endothelial cell;
KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
KW anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug;
KW prognosis; inflammation; regeneration; wounded tissue; targetting;
KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;

KW occlusive thrombus.
XX
OS Synthetic.
XX
PN WO9913329-A1.
XX
PD 18-MAR-1999.
XX
PF 08-SEP-1998; 98WO-US018895.
XX
PR 10-SEP-1997; 97US-00926914.
PR 25-AUG-1998; 98US-00139802.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti E, Pasqualini R;
XX
DR WPI; 1999-215158/18.
XX
PT Identifying molecules that home to angiogenic vasculature used as targets
PT for anticancer agents.
XX
PS Claim 15; Page 7; 180pp; English.
XX
CC This invention describes novel peptides which home to angiogenic
CC vasculature, specifically of a tumour and which have anti-tumour, anti-
CC inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules
CC are identified by treating a purified NGR receptor with a test compound
CC and identifying compounds that bind specifically to the NGR receptor. The
CC peptides of the invention are inhibitors of angiogenesis and can be used
CC to produce conjugates for delivering agents to angiogenic vasculature,
CC particularly anticancer drugs or an imaging agent, for diagnosis or
CC prognosis. These conjugates may be directed to non-tumour angiogenic
CC vasculature, e.g. that present in inflammatory, regenerating or wounded
CC tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
CC or rheumatoid arthritis. The peptides provide specific targeting to
CC tumours, especially their supporting vasculature, since the NGR receptor
CC is exposed to the circulation only in angiogenic vasculature. Precise
CC targeting should reduce the systemic toxicity of anticancer drugs in the
CC conjugates. Complete killing of all target cells may not be essential
CC since partial denudation of endothelium may result in an occlusive
CC thrombus, and endothelial cells are unlikely tc become resistant to
CC anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and
CC AAW93843-44 are examples of tumour homing peptides used in the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 7
AAY48821
ID AAY48821 standard; peptide; 9 AA.
XX
AC AAY48821;
XX
DT 20-MAR-2003 (revised)
DT 10-DEC-1999 (first entry)
XX
DE Membrane dipeptidase-binding retina homing peptide #7.
XX
KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW membrane dipeptidase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9946284-A2.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US005284.
XX
PR 13-MAR-1998; 98US-00042107.
PR 26-FEB-1999; 99US-00258754.
XX
PA (BURN-) BURNHAM INST.
XX
PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX
DR WPI; 1999-571717/48.
XX
PT New peptides which selectively home to organs or tissues, used for, e.g.
PT identifying target ligands and for therapy of pathological conditions.
XX
PS Example 6; Page 149; 193pp; English.
XX
CC The present invention describes peptides that selectively home to a
CC tissue or organ. The peptides can be used for identifying an organ or
CC tissue, for identifying a target molecule expressed by an organ or tissue
CC or for treating an organ or tissue pathology, where the organ or tissue
CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
CC used in the exemplification of the present invention. (Updated on 20-MAR-
CC 2003 to correct PR field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 8
AAY54271
ID AAY54271 standard; peptide; 9 AA.
XX
AC AAY54271;
XX
DT 06-APR-2000 (first entry)
XX
DE Alpha Vbeta-3 binding peptide sequence.
XX
KW Envelope protein; mutant; retrovirus; surface protein shedding;
KW envelope protein stability; gene therapy; drug therapy; cancer;
KW adenosine deaminase deficiency; thalassemia; hemophilia; diabetes;
KW alpha-anti trypsin deficiency; brain disorder; neural disorder;
KW phenylketonuria; growth disorder; heart disease; immune disease.
XX
OS Unidentified.
XX
PN WO9960110-A2.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011155.
XX
PR 20-MAY-1998; 98US-0086149P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
XX
PI Albritton LM, Zavorotinskaya T;
XX
DR WPI; 2000-116313/10.

XX
PT Novel isolated nucleic acid, useful for gene therapy.
XX
PS Example 10; Page 84; 190pp; English.
XX
CC The specification describes mutant retrovirus envelope proteins. The
CC envelope protein coding sequence can be mutated to encode a mutant
CC envelope protein with a substitution of one or more amino acids in at
CC least one motif of the retrovirus protein. The mutant protein fragment
CC allows for decreased shedding of the surface protein by suppressing
CC precursor cleavage and increase envelope stability and fusion of
CC retroviruses with cell membranes, while maintaining mutant envelope
CC protein incorporation into a virion, and viral titers of about two orders
CC of magnitude within that observed for wild-type retrovirus when the
CC protein or fragment is expressed on the surface of a retroviral particle.
CC The proteins have an increased ability to penetrate targets, typically
CC cells and a correspondingly increased ability to deliver nucleic acids or
CC drugs. The mutated nucleic acid is useful for gene and drug therapy,
CC especially as drug delivery vehicles. The retrovirus particles can be
CC utilized to transduce eukaryotic cells. The transduced cells are useful
CC in the treatment of cancer in a human. Other diseases contemplated for
CC treatment include adenosine deaminase deficiency (ADA), thalassemia,
CC hemophilia, diabetes, alpha-anti trypsin deficiency, brain and neural
CC disorders, phenylketonuria, growth disorders, heart diseases and immune
CC diseases. The present sequence was used in the course of the invention,
CC to quantitate targeted retroviral vector gene delivery in vivo
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 9
AAY44970
ID AAY44970 standard; protein; 9 AA.
XX
AC AAY44970;
XX
DT 23-MAY-2000 (first entry)
XX
DE RGD-4C targeting sequence for KDEL receptor inhibitor protein.
XX
KW KDEL receptor inhibitor; heat shock protein; immune response;
KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
KW melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
KW infectious disease; allergy; autoimmune disease.
XX
OS Unidentified.
XX
PN WO200006729-A1.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-US017147.
XX
PR 29-JUL-1998; 98US-00124671.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Rothman JE, Mayhew M, Hoe MH;
XX
DR WPI; 2000-195296/17.
XX
PT Inhibitors of the KDEL receptor which comprises an oligomerization domain
PT useful for promoting secretion of proteins which are normally retained
PT within the cell.
XX
PS Disclosure; Page 17; 87pp; English.
XX
CC The patent discloses the use of KDEL receptor inhibitor to promote
CC secretion of proteins that are normally retained within the cell such as
CC heat shock proteins by inhibiting KDEL receptor-mediated return of
CC protein complexes to endoplasmic reticulum. This makes the secreted heat
CC shock proteins more accessible to the immune system and improves immune
CC response to a target antigen. The inhibitor protein comprises several
CC subunits where each subunit comprises an oligomerisation domain and has
CC at its carboxy terminus a region which binds to a KDEL receptor. The
CC target antigen may be associated with diseases including neoplasia such
CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
CC astromytoma, with defective tumour suppressor genes, oncogenes,
CC infectious diseases, allergy or autoimmune diseases. The present sequence
CC is a targeting peptide termed RGD-4C. This may be incorporated into the
CC amino terminal region of a KDEL receptor inhibitor protein downstream
CC from a cleavably removed sequence to improve its activity or alter its
CC immunogenicity
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 10
AAB17928
ID AAB17928 standard; peptide; 9 AA.
XX
AC AAB17928;
XX
DT 31-OCT-2000 (first entry)
XX
DE TPO-mimetic peptide sequence SEQ ID NO:1032.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Disclosure; Page 559; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 11
AAB17964
ID AAB17964 standard; peptide; 9 AA.
XX
AC AAB17964;
XX
DT 31-OCT-2000 (first entry)
XX
DE Integrin-binding peptide sequence SEQ ID NO:1076.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 591; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 12
AAB17346
ID AAB17346 standard; peptide; 9 AA.
XX
AC AAB17346;
XX
DT 31-OCT-2000 (first entry)
XX
DE Integrin-binding peptide sequence SEQ ID NO:450.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 354; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 13
AAY90211
ID AAY90211 standard; peptide; 9 AA.
XX
AC AAY90211;
XX
DT 06-AUG-2003 (revised)
DT 21-SEP-2000 (first entry)
XX
DE Alphav integrin targeting peptide #1.
XX
KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;
KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
KW smooth muscle cell proliferation inhibitor; coronary artery disease;
KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
KW thrombosis; diabetes; tropism-modified virus.
XX
OS Synthetic.
XX
PN WO200012738-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-IB001524.
XX
PR 27-AUG-1998; 98US-0098028P.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;
XX
DR WPI; 2000-256653/22.
XX
PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
PT vectors having modified hexon HRV5 and HI loops and modified fiber
PT proteins useful for targeted gene therapy to treat cancer or restenosis.
XX
PS Example 5; Page 53; 128pp; English.
XX
CC This sequence represents a alphav integrin targeting peptide. The
CC invention relates to an adenovirus from which at least a part of the
CC hexon HVR5 or HI loop is replaced with a binding peptide, or targeting
CC sequence, flanked by connecting amino acid spacers, to functionally
CC display its binding specificity at the capsid surface. The invention also
CC relates to a recombinant adenovirus vector where a binding peptide, or
CC targeting sequence, is connected to the C-terminus of the fiber by a
CC connecting spacer, or linker, so as to functionally display its binding
CC specificity at the capsid surface. The adenovirus or recombinant
CC adenovirus vector can be used to preferentially express a gene in a
CC target cell, especially a cell that expresses a UPAR. The targeted
CC adenovirus vector preferably comprises a heterologous gene encoding a
CC gene for treatment of a tumour or restenosis. The targeted adenovirus
CC vector is useful for gene therapy treatment of a disease, and for
CC manufacturing a medicine used in gene therapy treatment of a disease. The
CC viruses can also be used to inhibit smooth muscle cell proliferation, to
CC treat peripheral artery diseases, coronary artery diseases, obesity,
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
CC thrombosis, and diabetes. The viruses are particularly targeted against a
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
CC are tropism-modified without adversely impacting productivity of the
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 14
AAO22875
ID AAO22875 standard; peptide; 9 AA.
XX
AC AAO22875;
XX
DT 30-JAN-2003 (first entry)
XX
DE Angiogenic treatment compound related synthetic peptide #75.
XX
KW Cyclic; cytostatic; antitumour; targeting moiety; chelator; peptide;
KW peptidomimetic; angiogenesis; metallopharmaceutical; new blood vessel;
KW rheumatoid arthritis; cancer; cancer planar; SPECT gamma scintigraphy;
KW positron emission; X-ray computed tomography; magnetic resonance imaging;
KW synthetic cyclic peptide.
XX
OS Synthetic.
XX
PN WO9958162-A2.
XX
PD 18-NOV-1999.
XX
PF 29-MAR-1999; 99WO-US006826.
XX
PR 31-MAR-1998; 98US-0080150P.
PR 18-DEC-1998; 98US-0112715P.
XX
PA (DUPO) DU PONT PHARM CO.
XX
PI Rajopadhye M, Edwards DS, Harris TD, Heminway SJ, Liu S;
PI Singh PR;
XX
DR WPI; 2000-105546/09.
XX
PT Novel compound for diagnosis and treatment of cancer.
XX
PS Disclosure; Page 62; 213pp; English.
XX
CC The invention relates to compounds comprising targeting moiety which is
CC bound to a chelator. The targeting moiety is a peptide or peptidomimetic
CC which binds to a receptor and is upregulated during angiogenesis. The
CC compound has 0-1 linking groups between targeting moiety and the
CC chelator. The metallopharmaceutical composition is used in treating
CC rheumatoid arthritis or cancer by imaging the formation of new blood
CC vessels, imaging cancer planar or SPECT gamma scintigraphy, positron
CC emission or X-ray computed tomography or with magnetic resonance imaging.
CC This sequence represents a synthetic cyclic peptide relating to the novel
CC compounds of the invention
XX
SQ Sequence 9 AA;

```
  Query Match             100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 15
AAB21701
ID   AAB21701 standard; peptide; 9 AA.
XX
AC   AAB21701;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human breast tumour homing peptide #1.
XX
KW   Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW   breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
XX
OS   Homo sapiens.
XX
PN   WO200042973-A2.
XX
PD   27-JUL-2000.
XX
PF   21-JAN-2000; 2000WO-US001602.
XX
PR   22-JAN-1999;   99US-00235902.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Ellerby HM,  Bredesen DE,  Pasqualini R,  Ruoslahti EI;
XX
DR   WPI; 2000-499174/44.
XX
PT   Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT   selectively homes to a mammalian cell type or tissue linked to an
PT   antimicrobial peptide, useful for the treatment of prostate cancer.
XX
PS   Claim 12; Page 105; 118pp; English.
XX
CC   The present invention relates to homing pro-apoptotic conjugates,
CC   comprising of a tumour homing molecule that selectively homes to a
CC   mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC   homing pro-apoptotic conjugates are selectively internalised by the
CC   mammalian cell type or tissue and exhibits high toxicity, especially to
CC   angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC   toxicity when not linked to the tumor homing molecule. The conjugates are
CC   useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC   prostate cancer or melanoma. The present sequence is a homing peptide
CC   isolated in the present invention, which can be conjugated to an
CC   antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC   present invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


Search completed: July 11, 2004, 09:16:06
Job time : 58 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:16:11 ; Search time 47 Seconds
(without alignments)
59.729 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	65	100.0	9	9	US-09-765-086-1	Sequence 1, Appli
2	65	100.0	9	9	US-09-845-160-5	Sequence 5, Appli
3	65	100.0	9	9	US-09-245-603A-16	Sequence 16, Appl
4	65	100.0	9	9	US-09-364-597A-16	Sequence 16, Appl
5	65	100.0	9	9	US-09-734-628-1	Sequence 1, Appli
6	65	100.0	9	9	US-09-971-798-5	Sequence 5, Appli
7	65	100.0	9	9	US-09-969-192-3	Sequence 3, Appli
8	65	100.0	9	9	US-09-840-277-38	Sequence 38, Appl
9	65	100.0	9	9	US-09-840-277-62	Sequence 62, Appl
10	65	100.0	9	10	US-09-801-485-2	Sequence 2, Appli
11	65	100.0	9	10	US-09-791-524-124	Sequence 124, App
12	65	100.0	9	12	US-10-609-217-450	Sequence 450, App
13	65	100.0	9	12	US-10-609-217-1076	Sequence 1076, Ap
14	65	100.0	9	12	US-10-363-208-166	Sequence 166, App
15	65	100.0	9	12	US-10-632-388-450	Sequence 450, App
16	65	100.0	9	12	US-10-632-388-1076	Sequence 1076, Ap
17	65	100.0	9	12	US-10-652-244-20	Sequence 20, Appl
18	65	100.0	9	12	US-10-651-723-450	Sequence 450, App
19	65	100.0	9	12	US-10-651-723-1076	Sequence 1076, Ap
20	65	100.0	9	12	US-09-912-609-31	Sequence 31, Appl
21	65	100.0	9	12	US-09-995-388-47	Sequence 47, Appl
22	65	100.0	9	12	US-10-013-009-1	Sequence 1, Appli
23	65	100.0	9	12	US-10-033-769-10	Sequence 10, Appl
24	65	100.0	9	12	US-10-269-575-1	Sequence 1, Appli
25	65	100.0	9	12	US-10-645-761-450	Sequence 450, App
26	65	100.0	9	12	US-10-645-761-1076	Sequence 1076, Ap
27	65	100.0	9	13	US-10-080-854-8	Sequence 8, Appli
28	65	100.0	9	13	US-10-038-972A-10	Sequence 10, Appl
29	65	100.0	9	14	US-10-304-160-3	Sequence 3, Appli
30	65	100.0	9	14	US-10-264-374-1	Sequence 1, Appli
31	65	100.0	9	14	US-10-032-221B-35	Sequence 35, Appl
32	65	100.0	9	14	US-10-375-992-1	Sequence 1, Appli
33	65	100.0	9	16	US-10-666-696-450	Sequence 450, App
34	65	100.0	9	16	US-10-666-696-1076	Sequence 1076, Ap
35	65	100.0	9	16	US-10-653-048-450	Sequence 450, App
36	65	100.0	9	16	US-10-653-048-1076	Sequence 1076, Ap
37	65	100.0	9	16	US-10-264-374-1	Sequence 1, Appli
38	65	100.0	10	9	US-09-845-160-14	Sequence 14, Appl
39	65	100.0	10	9	US-09-870-203A-43	Sequence 43, Appl
40	65	100.0	10	12	US-09-780-142-2	Sequence 2, Appli
41	65	100.0	10	14	US-10-429-496-2	Sequence 2, Appli
42	65	100.0	10	14	US-10-429-428-2	Sequence 2, Appli
43	65	100.0	10	15	US-10-403-337-30	Sequence 30, Appl
44	65	100.0	10	15	US-10-351-890-30	Sequence 30, Appl
45	65	100.0	10	15	US-10-296-879-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-765-086-1
; Sequence 1, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9

RESULT 2
US-09-845-160-5

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; Sequence 5, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
;  APPLICANT: MIZUGUCHI, HIROYUKI
;  APPLICANT:  HAYAKAWA, TAKAO
;  TITLE OF INVENTION: ADENOVIRUS VECTOR
;  FILE REFERENCE: 081356/0163
;  CURRENT APPLICATION NUMBER: US/09/845,160
;  CURRENT FILING DATE:  2001-05-01
;  PRIOR APPLICATION NUMBER: JP 2001-131688
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: JP 2000-161577
;  PRIOR FILING DATE: 2000-05-31
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide.
US-09-845-160-5

  Query Match           100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 3
US-09-245-603A-16
; Sequence 16, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
;  APPLICANT:  Curiel, David T.
;  APPLICANT:  Krasnykh, Victor N.
;  APPLICANT:  Dmitriev, Igor
;  TITLE OF INVENTION:  Adenovirus Vector Containing A Heterologous Peptide
;  TITLE OF INVENTION:  Epitope in the HI Loop of the Fiber Knob
;  FILE REFERENCE:  D6080
;  CURRENT APPLICATION NUMBER: US/09/245,603A
;  CURRENT FILING DATE:  1999-02-05
;  PRIOR APPLICATION NUMBER:  US 60/099,801
;  PRIOR FILING DATE:  1998-09-10
;  NUMBER OF SEQ ID NOS:  17
; SEQ ID NO 16
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
;   OTHER INFORMATION: into the region of the fiber gene within the HI loop.
US-09-245-603A-16

  Query Match           100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 4
US-09-364-597A-16
; Sequence 16, Application US/09364597A
; Patent No. US20020103130A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ruoslahti, Erkki
;    APPLICANT:  Koivunen, Erkki
;    TITLE OF INVENTION:  No. US20020103130A1el Integrin-Binding Peptides
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/364,597A
;      FILING DATE:  30-JUL-1999
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/158,001
;      FILING DATE:  24-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/286,861
;      FILING DATE:  04-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 3419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (858) 535-9001
;      TELEFAX:  (858) 535-8949
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  circular
US-09-364-597A-16

  Query Match           100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 5
US-09-734-628-1
; Sequence 1, Application US/09734628
; Patent No. US20020122806A1
; GENERAL INFORMATION:
;  APPLICANT: Chinnaiyan, Arul M.
;  APPLICANT:  Rehemtulla, Alnawaz
;  APPLICANT:  Ross, Brian D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IN SITU AND
;  TITLE OF INVENTION:  IN VIVO IMAGING OF CELLS AND TISSUES
;  FILE REFERENCE: 11203-005001
;  CURRENT APPLICATION NUMBER: US/09/734,628
;  CURRENT FILING DATE:  2000-12-11
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-09-734-628-1

  Query Match           100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CDCRGDCFC 9
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Db          1 CDCRGDCFC 9


RESULT 6
US-09-971-798-5
; Sequence 5, Application US/09971798
; Patent No. US20020132769A1
; GENERAL INFORMATION:
;  APPLICANT: No. US20020132769A1artis AG
;  TITLE OF INVENTION: Targeting molecules
;  FILE REFERENCE: 4-31615/GTI
;  CURRENT APPLICATION NUMBER: US/09/971,798
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-971-798-5

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
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Db          1 CDCRGDCFC 9


RESULT 7
US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. US20020151027A1
;   GENERAL INFORMATION:
;        APPLICANT: WICKHAM, THOMAS J.
;                   ROELVINK, PETRUS W.
;                   KOVESDI, IMRE
;        TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                            CONSTRAINED PEPTIDE MOTIFS
;        NUMBER OF SEQUENCES: 80
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;             STREET: Two Prudential Plaza - 49th Floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/969,192
;             FILING DATE: 01-Oct-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 9-455061
;             FILING DATE: 06-DEC-1999
;             APPLICATION NUMBER: US 9-130225
;             FILING DATE: 06-AUG-1998
;             APPLICATION NUMBER: US 8-701124
;             FILING DATE: 21-AUG-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hefner, M. Daniel
;             REGISTRATION NUMBER: 41,826
;             REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 8
US-09-840-277-38
; Sequence 38, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-38

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
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Db          1 CDCRGDCFC 9


RESULT 9
US-09-840-277-62
; Sequence 62, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 9
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-62

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 10
US-09-801-485-2
; Sequence 2, Application US/09801485
; Publication No. US20030077818A1
; GENERAL INFORMATION:
;  APPLICANT:  Dickerson, Erin B
;  APPLICANT:  Helfand, Stuart C.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TARGETING INTERLEUKIN-12
;  TITLE OF INVENTION:  TO MALIGNANT ENDOTHELIUM
;  FILE REFERENCE:  WARF-0003
;  CURRENT APPLICATION NUMBER: US/09/801,485
;  CURRENT FILING DATE:  2001-03-08
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-801-485-2

  Query Match             100.0%;  Score 65;  DB 10;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
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Db          1 CDCRGDCFC 9


RESULT 11
US-09-791-524-124
; Sequence 124, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
;  APPLICANT:  Aventis Pharmaceuticals Products Inc.
;  TITLE OF INVENTION:  Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
;  FILE REFERENCE:  A3319A
;  CURRENT APPLICATION NUMBER: US/09/791,524
;  CURRENT FILING DATE:  2001-02-22
;  PRIOR APPLICATION NUMBER:  60/09828
;  PRIOR FILING DATE:  1998-08-27
;  NUMBER OF SEQ ID NOS:  150
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 124
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Adenovirus
US-09-791-524-124

  Query Match             100.0%;  Score 65;  DB 10;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 12
US-10-609-217-450
; Sequence 450, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-450

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 13
US-10-609-217-1076
; Sequence 1076, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1076

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9
```

RESULT 14
US-10-363-208-166
; Sequence 166, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-166

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 15
US-10-632-388-450
; Sequence 450, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-450

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

Search completed: July 11, 2004, 09:21:50
Job time : 48 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:17:42 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	32.3	9	1	COW_CONVE	P83047 conus ventr
2	16	24.6	7	1	BRHP_CONIM	P58803 conus imper
3	15	23.1	7	1	FAR1_HELTI	P41871 helisoma tr
4	15	23.1	8	1	ACT_CARMA	P80709 carcinus ma
5	15	23.1	9	1	CCAP_CARMA	P38556 carcinus ma
6	15	23.1	9	1	CONO_CONGE	P05486 conus geogr
7	15	23.1	9	1	OXYT_EISFO	P42998 eisenia foe
8	15	23.1	9	1	SAP_STOVA	P24047 stomopneute
9	13	20.0	9	1	DSIP_RABIT	P01158 oryctolagus
10	13	20.0	9	1	TAL1_PICJA	P17440 pichia jadi
11	12	18.5	4	1	OCP1_OCTMI	P58648 octopus min
12	12	18.5	5	1	UXA4_CHLTR	P38005 chlamydia t
13	12	18.5	7	1	PPH2_LYCES	P83379 lycopersico
14	12	18.5	8	1	ACI_THUAL	P18691 thunnus alb
15	12	18.5	8	1	FAR1_PENMO	P83316 penaeus mon
16	12	18.5	8	1	LMT2_LOCMI	P22396 locusta mig
17	12	18.5	8	1	ORMY_ORCLI	P82455 orconectes
18	12	18.5	9	1	ISOT_CYPCA	P42993 cyprinus ca
19	12	18.5	9	1	OXYA_SCYCA	P42996 scyliorhinu
20	12	18.5	9	1	OXYA_SQUAC	P42999 squalus aca
21	12	18.5	9	1	OXYF_SCYCA	P42997 scyliorhinu
22	12	18.5	9	1	OXYT_BUFRE	P42995 bufo regula
23	12	18.5	9	1	OXYT_CYPCA	P23879 cyprinus ca
24	12	18.5	9	1	OXYT_OCTVU	P80027 octopus vul
25	12	18.5	9	1	OXYT_RABIT	P32878 oryctolagus
26	12	18.5	9	1	OXYT_RAJCL	P42994 raja clavat
27	12	18.5	9	1	OXYV_SQUAC	P43000 squalus aca
28	12	18.5	9	1	PPH1_LYCES	P83380 lycopersico
29	12	18.5	9	1	UPA6_HUMAN	P30092 homo sapien
30	11	16.9	6	1	FARP_MONEX	P41966 moniezia ex
31	11	16.9	7	1	UF04_MOUSE	P38642 mus musculu
32	11	16.9	8	1	ALL5_CYDPO	P82156 cydia pomon
33	11	16.9	8	1	GLUR_HUMAN	P02729 homo sapien
34	11	16.9	9	1	CONO_CONST	P05487 conus stria
35	11	16.9	9	1	DNF1_LOCMI	P16339 locusta mig
36	11	16.9	9	1	FIBB_PAPAN	P19344 papio anubi
37	11	16.9	9	1	PGLR_DIAAB	P81179 diaprepes a
38	11	16.9	9	1	ULAH_HUMAN	P31934 homo sapien
39	10	15.4	5	1	RE11_LITRU	P82070 litoria rub
40	10	15.4	8	1	COW2_CONPU	P58785 conus purpu
41	10	15.4	8	1	RS1_ERWCH	P37985 erwinia chr
42	10	15.4	9	1	TAL3_PICJA	P17441 pichia jadi
43	9	13.8	7	1	FARB_CALVO	P41866 calliphora
44	9	13.8	8	1	CCKN_MACEU	P30369 macropus eu
45	9	13.8	8	1	LCK5_LEUMA	P19987 leucophaea

ALIGNMENTS

RESULT 1
COW_CONVE
ID COW_CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Polticelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT snail Conus ventricosus.";
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
RN [2]
RP STRUCTURE BY NMR, SYNTHESIS, DISULFIDE BONDS, AND FUNCTION.
RX MEDLINE=22533239; PubMed=12646193;
RA Massilia G.R., Eliseo T., Grolleau F., Lapied B., Barbier J.,
RA Bournaud R., Molgo J., Cicero D.O., Paci M., Schinina M.E.,
RA Ascenzi P., Polticelli F.;
RT "Contryphan-Vn: a modulator of Ca2+-dependent K+ channels.";
RL Biochem. Biophys. Res. Commun. 303:238-246(2003).
CC -!- FUNCTION: Affects both voltage-gated and calcium-dependent
CC potassium channel activities, with composite and diversified
CC effects in invertebrate and vertebrate systems.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: The cis isomer is the most abundant and is thus thought to be
CC the functionally relevant conformer.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the contryphan family.
DR PDB; 1NXN; 04-MAR-03.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor; D-amino acid; Amidation; 3D-structure.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 32.3%; Score 21; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          5 GDC 7
              |||
Db          1 GDC 3
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RESULT 2

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BRHP_CONIM
ID   BRHP_CONIM     STANDARD;      PRT;     7 AA.
AC   P58803;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bromoheptapeptide Im.
OS   Conus imperialis (Imperial cone).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC   Neogastropoda; Conoidea; Conidae; Conus.
OX   NCBI_TaxID=35631;
RN   [1]
RP   SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC   TISSUE=Venom;
RX   MEDLINE=97184108; PubMed=9030520;
RA   Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA   Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
RA   McIntosh J.M.;
RT   "A novel post-translational modification involving bromination of
RT   tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT   peptides from Conus imperialis and Conus radiatus venom.";
RL   J. Biol. Chem. 272:4689-4698(1997).
CC   -!- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC       centrally or peripherally in mice.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC   -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
DR   PIR; A58512; A58512.
KW   Bromination; Amidation; Pyrrolidone carboxylic acid.
FT   DISULFID      2      7
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       6      6       BROMINATION.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  795 MW;  6EA37DC6D87EA6B0 CRC64;

  Query Match             24.6%;  Score 16;  DB 1;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GDCFC 9
              |  :|
Db          3 GQAWC 7


RESULT 3
FAR1_HELTI
ID   FAR1_HELTI     STANDARD;      PRT;     7 AA.
AC   P41871;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide GDPFLRF-amide.
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC   Lymnaeoidea; Planorbidae; Helisoma.
OX   NCBI_TaxID=27815;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: Appears to be involved in osmoregulation by affecting
CC       the kidney, mantle and skin.
CC   -!- TISSUE SPECIFICITY: Kidney, skin, mantle and the hemolymph.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  851 MW;  69D40729D76AA810 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GDCF 8
              || |
Db          1 GDPF 4


RESULT 4
ACT_CARMA
ID   ACT_CARMA      STANDARD;      PRT;     8 AA.
AC   P80709;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Actin (Fragment).
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RA   Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA   Baghdassarian D.;
RT   "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL   Endocrine 5:23-32(1996).
CC   -!- FUNCTION: Actins are highly conserved proteins that are involved
CC       in various types of cell motility and are ubiquitously expressed
CC       in all eukaryotic cells.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC       6.8, ITS MW IS: 46 kDa.
CC   -!- SIMILARITY: Belongs to the actin family.
DR   InterPro; IPR004001; Actin.
DR   InterPro; IPR004000; Actin_like.
DR   PROSITE; PS00406; ACTINS_1; PARTIAL.
DR   PROSITE; PS00432; ACTINS_2; PARTIAL.
DR   PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW   Structural protein.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  976 MW;  1424005AB2CAAEB3 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CD 2
              ||
Db          2 CD 3


RESULT 5
CCAP_CARMA
ID   CCAP_CARMA     STANDARD;      PRT;     9 AA.
AC   P38556;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cardioactive peptide (CCAP).
OS   Carcinus maenas (Common shore crab) (Green crab),
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS   Tenebrio molitor (Yellow mealworm), and
OS   Spodoptera eridania (Southern armyworm).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759, 7130, 7067, 37547;
RN   [1]
RP   SEQUENCE.
```

```
RC   SPECIES=C.maenas; TISSUE=Pericardial organs;
RA   Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT   "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT   shore crab Carcinus maenas.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=M.sexta;
RX   MEDLINE=93050243; PubMed=1426284;
RA   Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT   "Primary structure of a cardioactive neuropeptide from the tobacco
RT   hawkmoth, Manduca sexta.";
RL   FEBS Lett. 313:165-168(1992).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX   MEDLINE=94176032; PubMed=8129851;
RA   Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA   Schooley D.A.;
RT   "Isolation and identification of a cardioactive peptide from Tenebrio
RT   molitor and Spodoptera eridania.";
RL   Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC   -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Stored in pericardial organs and released
CC       into the hemolymph.
DR   PIR; A26363; A26363.
DR   PIR; S27233; S27233.
KW   Neuropeptide; Amidation.
FT   DISULFID       3       9
FT   MOD_RES        9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  959 MW;  C5A861A9CDD44EB9 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FC 9
              ||
Db          2 FC 3


RESULT 6
CONO_CONGE
ID   CONO_CONGE     STANDARD;      PRT;      9 AA.
AC   P05486;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Lys-conopressin G.
OS   Conus geographus (Geography cone).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC   Neogastropoda; Conoidea; Conidae; Conus.
OX   NCBI_TaxID=6491;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=88058932; PubMed=3680228;
RA   Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA   Gray W.R., Olivera B.M.;
RT   "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT   peptides from Conus geographus and Conus straitus venoms.";
RL   J. Biol. Chem. 262:15821-15824(1987).
RN   [2]
RP   REVIEW.
RX   MEDLINE=89024586; PubMed=3052286;
RA   Gray W.R., Olivera B.M., Cruz L.J.;
RT   "Peptide toxins from venomous Conus snails.";
RL   Annu. Rev. Biochem. 57:665-700(1988).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR   PIR; A28495; A28495.
DR   InterPro; IPR000981; Neurhyp_horm.
DR   Pfam; PF00220; hormone4; 1.
DR   PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW   Hormone; Amidation.
FT   DISULFID       1       6
FT   MOD_RES        9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1037 MW;  D4FC276EB4540059 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CF 8
              ||
Db          1 CF 2


RESULT 7
OXYT_EISFO
ID   OXYT_EISFO     STANDARD;      PRT;      9 AA.
AC   P42998;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Annetocin.
OS   Eisenia foetida (Common brandling worm) (Common dung-worm).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC   Lumbricina; Lumbricidae; Eisenia.
OX   NCBI_TaxID=6396;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pituitary;
RX   MEDLINE=94121660; PubMed=8292046;
RA   Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA   Nomoto K.;
RT   "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT   Eisenia foetida.";
RL   Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC   -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC       PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC       NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC       NEPHRIDIAL FUNCTION.
CC   -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR   PIR; PC2021; PC2021.
DR   InterPro; IPR000981; Neurhyp_horm.
DR   Pfam; PF00220; hormone4; 1.
DR   PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW   Hormone; Amidation.
FT   DISULFID       1       6
FT   MOD_RES        9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  996 MW;  D4EEB76EB45412C9 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CF 8
              ||
Db          1 CF 2


RESULT 8
SAP_STOVA
ID   SAP_STOVA      STANDARD;      PRT;      9 AA.
AC   P24047;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sperm-activating peptide (SAP).
OS   Stomopneutes variolaris (Sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
OC   Stomopneustes.
OX   NCBI_TaxID=7663;
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```
RN   [1]
RP   SEQUENCE, AND DISULFIDE BOND.
RC   TISSUE=Egg jelly;
RX   MEDLINE=92097763; PubMed=1756858;
RA   Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.;
RT   "Determination of the amino acid sequence of an intramolecular
RT   disulfide linkage-containing sperm-activating peptide by tandem mass
RT   spectrometry.";
RL   FEBS Lett. 294:179-182(1991).
CC   -!- FUNCTION: Cause stimulation of sperm respiration and motility
CC       through intracellular alkalinization, transient elevations of
CC       cAMP, cGMP and calcium levels in sperm cells, and transient
CC       activation and subsequent inactivation of the membrane form of
CC       guanylate cyclase.
FT   DISULFID      3      8
SQ   SEQUENCE   9 AA;  1010 MW;  C469B3387B076EB9 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 FC 9
              ||
Db          2 FC 3


RESULT 9
DSIP_RABIT
ID   DSIP_RABIT     STANDARD;      PRT;     9 AA.
AC   P01158;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Delta sleep-inducing peptide (DSIP).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77185324; PubMed=862769;
RA   Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA   Schoenenberger G.A.;
RT   "The delta sleep inducing peptide (DSIP). Comparative properties of
RT   the original and synthetic nonapeptide.";
RL   Experientia 33:548-552(1977).
RN   [2]
RP   SEQUENCE, AND SYNTHESIS.
RX   MEDLINE=79054421; PubMed=568769;
RA   Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT   "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
RT   analysis, sequence, synthesis and activity of the nonapeptide.";
RL   Pflugers Arch. 376:119-129(1978).
RN   [3]
RP   REVIEW.
RX   MEDLINE=87175129; PubMed=3550726;
RA   Graf M.V., Kastin A.J.;
RT   "Delta-sleep-inducing peptide (DSIP): an update.";
RL   Peptides 7:1165-1187(1986).
CC   -!- FUNCTION: When infused into the mesodiencephalic ventricle of
CC       recipient rabbits induces spindle and delta EEG activity and
CC       reduced motor activities.
CC   -!- MISCELLANEOUS: This peptide was obtained from dialysates of
CC       occipital venous sinus blood from rabbits kept asleep by electric
CC       stimulation of the thalamus.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 8 of March 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".
DR   PIR; A01422; QDRB.
SQ   SEQUENCE   9 AA;  849 MW;  DDD365BDDAA8787D CRC64;

  Query Match             20.0%;  Score 13;  DB 1;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 DCRGD 6
              |  |:
Db          5 DASGE 9


RESULT 10
TAL1_PICJA
ID   TAL1_PICJA     STANDARD;      PRT;     9 AA.
AC   P17440;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Transaldolase I (EC 2.2.1.2) (Fragment).
OS   Pichia jadinii (Yeast) (Candida utilis).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Pichia.
OX   NCBI_TaxID=4903;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77110646; PubMed=556924;
RA   Sun S.C., Joris L., Tsolas O.;
RT   "Purification of crystallization of transaldolase isozyme I and
RT   evidence for different genetic origin of isozymes I and III in
RT   Candida utilis.";
RL   Arch. Biochem. Biophys. 178:69-78(1977).
CC   -!- FUNCTION: Transaldolase is important for the balance of
CC       metabolites in the pentose-phosphate pathway.
CC   -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC       3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC   -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC   -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
DR   PIR; A12872; A12872.
DR   InterPro; IPR001585; Transaldolase.
DR   PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR   PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW   Transferase; Pentose shunt.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1008 MW;  274F31AF0EB1E058 CRC64;

  Query Match             20.0%;  Score 13;  DB 1;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CD 2
              |:
Db          5 CB 6


RESULT 11
OCP1_OCTMI
ID   OCP1_OCTMI     STANDARD;      PRT;     4 AA.
AC   P58648;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cardioactive peptides Ocp-1/Ocp-2.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-2 is a 1000 time less
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CC       active than Ocp-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES      2      2       D-PHENYLALANINE (IN OCP-1).
SQ   SEQUENCE   4 AA;  394 MW;  6AA879C810000000 CRC64;

  Query Match             18.5%;  Score 12;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GD 6
              ||
Db          3 GD 4


RESULT 12
UXA4_CHLTR
ID   UXA4_CHLTR     STANDARD;      PRT;     5 AA.
AC   P38005;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Unknown protein from 2D-page from elementary body (Fragment).
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=813;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=L2/434/Bu;
RA   Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA   Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
RA   Pallini V.;
RL   Submitted (SEP-1994) to Swiss-Prot.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR   Siena-2DPAGE; P38005; -.
FT   NON_TER      5      5
SQ   SEQUENCE   5 AA;  474 MW;  75BAA865AA800000 CRC64;

  Query Match             18.5%;  Score 12;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GD 6
              ||
Db          3 GD 4


RESULT 13
PPH2_LYCES
ID   PPH2_LYCES     STANDARD;      PRT;     7 AA.
AC   P83379;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP   GLYCOSYLATION.
RC   STRAIN=cv. Moneymaker; TISSUE=Seed;
RX   MEDLINE=22361242; PubMed=12473124;
RA   Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT   "Purification and characterization of two secreted purple acid
RT   phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT   esculentum) cell cultures.";
RL   Eur. J. Biochem. 269:6278-6286(2002).
CC   -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC       alcohol + phosphate.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Glycosylated.
CC   -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of
CC       purple acid phosphatase.
KW   Hydrolase; Glycoprotein.
FT   NON_TER      1      1
FT   NON_TER      7      7
SQ   SEQUENCE   7 AA;  810 MW;  672AA862C9C729A0 CRC64;

  Query Match             18.5%;  Score 12;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GD 6
              ||
Db          5 GD 6


RESULT 14
ACI_THUAL
ID   ACI_THUAL      STANDARD;      PRT;     8 AA.
AC   P18691;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-NOV-1990 (Rel. 16, Last annotation update)
DE   Angiotensin-converting enzyme inhibitor.
OS   Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8236;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Muscle;
RX   MEDLINE=88326322; PubMed=3415688;
RA   Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT   "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT   muscle.";
RL   Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR   PIR; A31570; A31570.
SQ   SEQUENCE   8 AA;  953 MW;  6AA863733051F1B7 CRC64;

  Query Match             18.5%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GD 6
              ||
Db          7 GD 8


RESULT 15
FAR1_PENMO
ID   FAR1_PENMO     STANDARD;      PRT;     8 AA.
AC   P83316;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   FMRFamide-like neuropeptide FLP1 (GDRNFLRF-amide).
OS   Penaeus monodon (Penoeid shrimp).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC   Penaeidae; Penaeus.
OX   NCBI_TaxID=6687;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Eyestalk;
RX   MEDLINE=21956277; PubMed=11959015;
RA   Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
```

RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 18.5%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GD 6
||
Db 1 GD 2

Search completed: July 11, 2004, 09:23:55
Job time : 12 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:20:57 ; Search time 38 Seconds
(without alignments)
74.728 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	36.9	8	6	Q9TRY3	Q9try3 sus sp. ins
2	22	33.8	9	15	O12096	O12096 caprine art
3	22	33.8	9	15	O12100	O12100 caprine art
4	22	33.8	9	15	O12102	O12102 caprine art
5	22	33.8	9	15	O12098	O12098 caprine art
6	22	33.8	9	15	O12104	O12104 caprine art
7	19.5	30.0	9	10	Q9FSZ2	Q9fsz2 cicer ariet
8	19.5	30.0	9	11	Q99JF4	Q99jf4 mus musculu
9	19	29.2	7	11	O55184	O55184 rattus norv
10	17	26.2	8	4	Q9BYY5	Q9byy5 homo sapien
11	17	26.2	8	6	Q9BF82	Q9bf82 ursus arcto
12	17	26.2	8	6	Q9BFC2	Q9bfc2 macropus eu
13	17	26.2	8	6	Q9BF90	Q9bf90 tragelaphus
14	17	26.2	8	6	Q9BFB1	Q9bfb1 echinops te
15	17	26.2	8	6	Q9BF93	Q9bf93 megaptera n
16	17	26.2	8	6	Q9BFA1	Q9bfa1 ateles fusc
17	17	26.2	8	6	Q9BF87	Q9bf87 tapirus ind
18	17	26.2	8	6	Q9BFB9	Q9bfb9 euphractus
19	17	26.2	8	6	Q9BFB8	Q9bfb8 chaetophrac
20	17	26.2	8	6	Q9BFA0	Q9bfa0 macaca mula
21	17	26.2	8	6	Q9BFA8	Q9bfa8 loxodonta a
22	17	26.2	8	6	Q9BFA9	Q9bfa9 procavia ca
23	17	26.2	8	6	Q9BFB2	Q9bfb2 sorex arane
24	17	26.2	8	6	Q9BFB5	Q9bfb5 erinaceus c
25	17	26.2	8	6	Q9BFB6	Q9bfb6 myrmecophag
26	17	26.2	8	6	Q9BFB3	Q9bfb3 condylura c
27	17	26.2	8	6	Q9BF88	Q9bf88 equus cabal
28	17	26.2	8	6	Q9BF95	Q9bf95 rousettus l
29	17	26.2	8	6	Q9BF99	Q9bf99 hylobates c
30	17	26.2	8	6	Q9BF84	Q9bf84 panthera on
31	17	26.2	8	6	Q9BFC3	Q9bfc3 didelphis m
32	17	26.2	8	6	Q9BFA4	Q9bfa4 tupaia mino
33	17	26.2	8	6	Q9BFA2	Q9bfa2 tarsius ban
34	17	26.2	8	6	Q9BF85	Q9bf85 leopardus p
35	17	26.2	8	6	Q9BFC1	Q9bfc1 choloepus h
36	17	26.2	8	6	Q9BF89	Q9bf89 okapia john
37	17	26.2	8	6	Q9BF96	Q9bf96 pteropus gi
38	17	26.2	8	6	Q9BFB0	Q9bfb0 trichechus
39	17	26.2	8	6	Q9BF86	Q9bf86 felis silve
40	17	26.2	8	6	Q9BF92	Q9bf92 tursiops tr
41	17	26.2	8	6	Q9BFB7	Q9bfb7 tamandua te
42	17	26.2	8	6	Q9BF91	Q9bf91 hippopotamu
43	17	26.2	8	6	Q9BFB4	Q9bfb4 talpa altai
44	17	26.2	8	6	Q9BFC0	Q9bfc0 choloepus d
45	17	26.2	8	6	Q9BF98	Q9bf98 callimico g

ALIGNMENTS

RESULT 1
Q9TRY3
ID Q9TRY3 PRELIMINARY; PRT; 8 AA.
AC Q9TRY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 36.9%; Score 24; DB 6; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GDCFC 9
| |:|
Db 2 GPCWC 6

RESULT 2
O12096
ID O12096 PRELIMINARY; PRT; 9 AA.
AC O12096;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE   Tat protein (Fragment).
GN   TAT.
OS   Caprine arthritis encephalitis virus (CAEV).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11660;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT   "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT   to A substitutions.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U81439; AAB60832.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  922 MW;  21E8644EB7340EB8 CRC64;

  Query Match             33.8%;  Score 22;  DB 15;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCR 4
              | ||
Db          1 CGCR 4


RESULT 3
O12100
ID   O12100      PRELIMINARY;      PRT;     9 AA.
AC   O12100;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Tat protein (Fragment).
GN   TAT.
OS   Caprine arthritis encephalitis virus (CAEV).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11660;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT   "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT   to A substitutions.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U81441; AAB60836.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  922 MW;  21E8644EB7340EB8 CRC64;

  Query Match             33.8%;  Score 22;  DB 15;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCR 4
              | ||
Db          1 CGCR 4


RESULT 4
O12102
ID   O12102      PRELIMINARY;      PRT;     9 AA.
AC   O12102;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Tat protein (Fragment).
GN   TAT.
OS   Caprine arthritis encephalitis virus (CAEV).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11660;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT   "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT   to A substitutions.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U81442; AAB60838.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  922 MW;  21E8644EB7340EB8 CRC64;

  Query Match             33.8%;  Score 22;  DB 15;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCR 4
              | ||
Db          1 CGCR 4


RESULT 5
O12098
ID   O12098      PRELIMINARY;      PRT;     9 AA.
AC   O12098;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Tat protein (Fragment).
GN   TAT.
OS   Caprine arthritis encephalitis virus (CAEV).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11660;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT   "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT   to A substitutions.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U81440; AAB60835.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  922 MW;  21E8644EB7340EB8 CRC64;

  Query Match             33.8%;  Score 22;  DB 15;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCR 4
              | ||
Db          1 CGCR 4


RESULT 6
O12104
ID   O12104      PRELIMINARY;      PRT;     9 AA.
AC   O12104;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Tat protein (Fragment).
GN   TAT.
OS   Caprine arthritis encephalitis virus (CAEV).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11660;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT   "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT   to A substitutions.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U81443; AAB60840.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  922 MW;  21E8644EB7340EB8 CRC64;

  Query Match             33.8%;  Score 22;  DB 15;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDCR 4
              | ||
Db          1 CGCR 4
```

```
RESULT 7
Q9FSZ2
ID   Q9FSZ2      PRELIMINARY;      PRT;     9 AA.
AC   Q9FSZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Cicer arietinum (Chickpea) (Garbanzo).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
OX   NCBI_TaxID=3827;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Castellana; TISSUE=Etiolated epicotyl;
RA   Dopico B., Jimenez T., Labrador E.;
RT   "cDNA clones expressed in etiolated Cicer arietinum epicotyls.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ299069; CAC10216.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  990 MW;  9441BDDAA7272EBE CRC64;

  Query Match             30.0%;  Score 19.5;  DB 10;  Length 9;
  Best Local Similarity   55.6%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 CDCRGD-CF 8
              | |  | ||
Db          1 CCCLLDACF 9


RESULT 8
Q99JF4
ID   Q99JF4      PRELIMINARY;      PRT;     9 AA.
AC   Q99JF4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Oct-1L (Fragment).
GN   OCT-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pankratova E.V., Deyev I.E., Zhenilo S.V., Polanovsky O.L.;
RT   "Tissue-specific Oct-1 isoforms from murine lymphocytes.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ310124; CAC34946.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  998 MW;  540BCEBAB5BEBAA7 CRC64;

  Query Match             30.0%;  Score 19.5;  DB 11;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          2 DCRGDC 7
              ||  ||
Db          3 DC-SDC 7


RESULT 9
O55184
ID   O55184      PRELIMINARY;      PRT;     7 AA.
AC   O55184;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orphan receptor TR4-NS (Fragment).
GN   TR4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96198747; PubMed=8612486;
RA   Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA   Detera-Wadleigh S.D.;
RT   "Splice variants of rat TR4 orphan receptor: differential expression
RT   of novel sequences in the 5'-untranslated region and C-terminal
RT   domain.";
RL   Endocrinology 137:1562-1571(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96299786; PubMed=8661150;
RA   Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT   "New variants of the human and rat nuclear hormone receptor, TR4:
RT   expression and chromosomal localization of the human gene.";
RL   Genomics 35:361-366(1996).
DR   EMBL; U59454; AAB91433.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  663 MW;  6DDAA8787EB05350 CRC64;

  Query Match             29.2%;  Score 19;  DB 11;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CRGD 6
              | ||
Db          3 CGGD 6


RESULT 10
Q9BYY5
ID   Q9BYY5      PRELIMINARY;      PRT;     8 AA.
AC   Q9BYY5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011664; AAG47575.1; -.
DR   GO; GO:0005634; C:nucleus; NAS.
DR   GO; GO:0003677; F:DNA binding; NAS.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1006 MW;  DF02C331EEAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 4;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4
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RESULT 11
Q9BF82
ID   Q9BF82      PRELIMINARY;      PRT;     8 AA.
AC   Q9BF82;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Ursus arctos (Brown bear) (Grizzly bear).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=9644;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011683; AAG47591.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  978 MW;  DF1DD331EEAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4


RESULT 12
Q9BFC2
ID   Q9BFC2      PRELIMINARY;      PRT;     8 AA.
AC   Q9BFC2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011621; AAG47536.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  978 MW;  DF1DD331EEAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4


RESULT 13
Q9BF90
ID   Q9BF90      PRELIMINARY;      PRT;     8 AA.
AC   Q9BF90;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Tragelaphus eurycerus (Bongo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Tragelaphus.
OX   NCBI_TaxID=69297;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011673; AAG47583.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  978 MW;  DF1DD331EEAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4


RESULT 14
Q9BFB1
ID   Q9BFB1      PRELIMINARY;      PRT;     8 AA.
AC   Q9BFB1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Echinops telfairi (Lesser hedgehog tenrec).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
OX   NCBI_TaxID=9371;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011632; AAG47547.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  978 MW;  DF1DD331EEAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4


RESULT 15
Q9BF93
ID   Q9BF93      PRELIMINARY;      PRT;     8 AA.
AC   Q9BF93;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cAMP responsive element moderator (Fragment).
GN   CREM.
OS   Megaptera novaeangliae (Humpback whale).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Megaptera.
OX   NCBI_TaxID=9773;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21082082; PubMed=11214319;
RA   Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA   O'Brien S.J.;
RT   "Molecular phylogenetics and the origins of placental mammals.";
RL   Nature 409:614-618(2001).
DR   EMBL; AY011669; AAG47580.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1025 MW;  DF02C3240EAB572A CRC64;

  Query Match             26.2%;  Score 17;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 DCFC 9
              | :|
Db          1 DLYC 4


Search completed: July 11, 2004, 09:24:46
Job time : 39 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 10:04:38 ; Search time 52 Seconds
(without alignments)
48.902 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	9	2	AAR76200	Aar76200 Alphav/be
2	65	100.0	9	2	AAW60289	Aaw60289 Tumour ho
3	65	100.0	9	2	AAW56034	Aaw56034 Chimeric
4	65	100.0	9	2	AAY42255	Aay42255 Synthetic
5	65	100.0	9	2	AAY43233	Aay43233 RGD-conta
6	65	100.0	9	2	AAW93626	Aaw93626 NGR recep
7	65	100.0	9	2	AAY48821	Aay48821 Membrane
8	65	100.0	9	3	AAY54271	Aay54271 Alpha Vbe
9	65	100.0	9	3	AAY44970	Aay44970 RGD-4C ta
10	65	100.0	9	3	AAB17928	Aab17928 TPO-mimet
11	65	100.0	9	3	AAB17964	Aab17964 Integrin-
12	65	100.0	9	3	AAB17346	Aab17346 Integrin-
13	65	100.0	9	3	AAY90211	Aay90211 Alphav in
14	65	100.0	9	3	AAO22875	Aao22875 Angiogeni
15	65	100.0	9	3	AAB21701	Aab21701 Human bre
16	65	100.0	9	4	AAB20271	Aab20271 Peptide t
17	65	100.0	9	4	AAB50242	Aab50242 Enhanced
18	65	100.0	9	4	AAB97086	Aab97086 Integrin-
19	65	100.0	9	4	AAE06279	Aae06279 Tumour ho
20	65	100.0	9	4	AAE11044	Aae11044 RGD-conta
21	65	100.0	9	5	AAU98837	Aau98837 Tumour ho
22	65	100.0	9	5	ABG35079	Abg35079 RGD-4C-be
23	65	100.0	9	5	AAU81110	Aau81110 Integrin-
24	65	100.0	9	5	AAU81134	Aau81134 Integrin-
25	65	100.0	9	5	ABP54051	Abp54051 Alpha-v-b
26	65	100.0	9	5	ABB72945	Abb72945 Integrin
27	65	100.0	9	5	ABB72961	Abb72961 Integrin
28	65	100.0	9	5	ABJ04359	Abj04359 BRASIL me
29	65	100.0	9	5	ABB08066	Abb08066 Cyclic RG
30	65	100.0	9	5	ABG70729	Abg70729 avB3 bind
31	65	100.0	9	5	ABB76442	Abb76442 RGD-4C Pe
32	65	100.0	9	5	AAE17983	Aae17983 Human lig
33	65	100.0	9	5	ABB78354	Abb78354 Amino aci
34	65	100.0	9	5	ABG70754	Abg70754 Targeting
35	65	100.0	9	5	AAU75609	Aau75609 Synthetic
36	65	100.0	9	5	AAU79138	Aau79138 Synthetic
37	65	100.0	9	5	AAU98972	Aau98972 Adeno-ass
38	65	100.0	9	5	AAM48795	Aam48795 Tumour-ta
39	65	100.0	9	5	ABB79525	Abb79525 RGD motif
40	65	100.0	9	5	ABG31063	Abg31063 Alpha v b
41	65	100.0	9	5	AAG78427	Aag78427 Cyclic pe
42	65	100.0	9	5	AAM51995	Aam51995 Drug targ
43	65	100.0	9	6	ABG73024	Abg73024 Integrin
44	65	100.0	9	6	ABB84641	Abb84641 Human int
45	65	100.0	9	6	ABU59556	Abu59556 Tumour an
46	65	100.0	9	6	ABU08571	Abu08571 RGD-conta
47	65	100.0	9	6	ABP60343	Abp60343 Tumour va
48	65	100.0	9	6	ADA20234	Ada20234 Synthetic
49	65	100.0	9	7	ADC44955	Adc44955 Endotheli

ALIGNMENTS

RESULT 1
AAR76200
ID AAR76200 standard; peptide; 9 AA.
XX
AC AAR76200;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alphav/beta3 and alphav/beta5 integrin binding peptide #4.
XX
KW High affinity; integrin binding peptide; alpha5/beta1; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachemnt; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
PN WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US013542.
XX
PR 24-NOV-1993; 93US-00158001.
PR 04-AUG-1994; 94US-00286861.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Ruoslahti E, Koivunen E;
XX
DR WPI; 1995-206899/27.
XX
PT High affinity integrin binding peptides - can be used to attach cells to
PT a substrate, inhibit the attachment of osteoclasts to bone, promote wound
PT healing, inhibit angiogenesis, metastasis of tumours and migration of
PT smooth muscle cells.
XX
PS Claim 21; Page 62; 86pp; English.
XX
CC The sequences given in AAR76185-200 and AAR79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides which
CC bind to alpha5/beta1 integrins contain the motifs given in AAR76185-86
CC and peptides which bind to alphav/beta5 and alphav/beta3 integrins
CC contain the motif given in AAR76187. Alphav/beta5 integrins are also

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CC   bound by RGD containing peptides. These peptides assume a
CC   conformationally stabilised configuration which is due to the formation
CC   of a disulphide bond, a peptide bond or a lactam bond. These peptides may
CC   be used for isolating the complementary integrin from a sample mixture by
CC   contacting them under ionic conditions to allow binding of the integrin
CC   to the peptide and then separating the integrin from the peptide. They
CC   can be used for attaching cells to a substrate, by binding them to the
CC   substrate with the cell. The peptides promote wound healing when applied
CC   locally and inhibit the attachment of osteoclasts to bone. They inhibit
CC   angiogenesis, metastasis of tumours and migration of smooth muscle cells
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 2
AAW60289
ID   AAW60289 standard; peptide; 9 AA.
XX
AC   AAW60289;
XX
DT   24-AUG-1998  (first entry)
XX
DE   Tumour homing peptide of the invention.
XX
KW   Tumour homing peptide; in vivo panning;
KW   alpha-V-containing integrin binding motif; tumour.
XX
OS   Unidentified.
XX
PN   WO9810795-A2.
XX
PD   19-MAR-1998.
XX
PF   10-SEP-1997;   97WO-US016086.
XX
PR   10-SEP-1996;   96US-00710067.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Ruoslahti E,  Pasqualini R;
XX
DR   WPI; 1998-207151/18.
XX
PT   Tumour homing molecules and their conjugates - useful for, e g. directing
PT   linked moiety to tumour containing angiogenic vasculature.
XX
PS   Claim 6; Page 91; 105pp; English.
XX
CC   The present peptide represents a tumour homing peptide, and is produced
CC   by in vivo panning. The peptide has an alpha-V-containing integrin
CC   binding motif, Arg-Gly-Asp (RGD). The in vivo panning comprises
CC   administering a library of diverse peptides to a subject having a tumour,
CC   collecting a sample of the tumour, identifying a peptide that homes to
CC   the tumour, collecting a sample of normal tissue corresponding to the
CC   tumour, and determining that the peptide that homes to the tumour is not
CC   present in the normal tissue. The tumour homing peptide can be linked to
CC   a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 3
AAW56034
ID   AAW56034 standard; peptide; 9 AA.
XX
AC   AAW56034;
XX
DT   29-JUL-1998  (first entry)
XX
DE   Chimeric adenovirus fiber protein non-native amino acid sequence 3.
XX
KW   Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW   constrained peptide motif; gene therapy; cancer; heart disease;
KW   autoimmune disorder.
XX
OS   Synthetic.
OS   Mastadenovirus.
XX
PN   WO9807865-A1.
XX
PD   26-FEB-1998.
XX
PF   21-AUG-1997;   97WO-US014719.
XX
PR   21-AUG-1996;   96US-00701124.
XX
PA   (GENV-) GENVEC INC.
XX
PI   Wickham TJ,  Roelvink PW,  Kovesdi I;
XX
DR   WPI; 1998-169169/15.
XX
PT   Chimeric adenovirus fibre proteins - containing non-native amino acid
PT   sequence to provide for binding and entry into cells, especially for gene
PT   therapy.
XX
PS   Claim 7; Page 68; 124pp; English.
XX
CC   The present sequence represents a specifically claimed non-native amino
CC   acid sequence from a chimeric adenovirus fibre protein (AFP) of the
CC   present invention. The non-native amino acid sequence allows the chimeric
CC   fibre (or a vector comprising the chimeric fibre) to more efficiently
CC   bind to and enter cells. The products can be used for gene therapy, for
CC   treating cancer, e.g. melanoma, glioma and lung cancers as well as
CC   genetic disorders, e.g. cystic fibrosis, haemophilia and muscular
CC   dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and
CC   hepatitis and also for heart disease, to e.g. prevent restenosis
CC   following angioplasty or to promote angiogenesis to reperfuse necrotic
CC   tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,
CC   rheumatoid arthritis, and Alzheimer's disease
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 4
AAY42255
ID   AAY42255 standard; peptide; 9 AA.
XX
AC   AAY42255;
XX
DT   01-DEC-1999  (first entry)
XX
```

DE Synthetic RGD-4C peptide.
XX
KW Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;
KW cancer; cystic fibrosis; muscular dystrophy.
XX
OS Synthetic.
XX
PN WO9939734-A1.
XX
PD 12-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US002549.
XX
PR 06-FEB-1998; 98US-0073947P.
PR 10-SEP-1998; 98US-0099801P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Curiel DT, Krasnykh VN, Dmitriev I;
XX
DR WPI; 1999-539951/45.
XX
PT Recombinant adenovirus vectors with modified fiber knob loops, useful in
PT gene therapy.
XX
PS Example 21; Page 49; 126pp; English.
XX
CC This sequence represents a synthetic RGD-4C peptide. DNA encoding this
CC sequence was cloned into the sequence encoding the HI loop of the
CC adenovirus fibre protein knob domain. This was then used in the
CC construction of plasmids encoding a modified fibre protein. Recombinant
CC adenovirus genomes were generated by homologous DNA recombination in E.
CC coli, before excision of the newly generated genome for virus rescue. The
CC knob domain of the adenovirus fibre protein mediates the initial binding
CC and recognition of the coxsackievirus and adenovirus receptor (CAR) on
CC the cell surface. The HI loop protrudes from the knob domain and connects
CC beta-strands involved in the formation of the cell binding site.
CC Recombinant adenovirus vectors are used in a number of gene therapy
CC applications; however, the reliance on the CAR means that in certain
CC situations, recombinant virions are sequestered by high CAR-expressing
CC non-target cells while the true target cells, if low in CAR, receive
CC little of the therapeutic gene. Modification of the HI loop by
CC replacement of the hypervariable region of the loop with a peptide such
CC as the RGD peptide results in the ability of the virus to utilise an
CC alternative receptor during the cell entry process. Modifying the
CC adenovirus fibre knob protein in this way increases the ability of an
CC adenovirus to transduce a tumour cell in vitro, in vivo and ex vivo. The
CC vector Ad5FHIFLAG incorporating an RGD peptide demonstrated two to three
CC orders of magnitude of increased gene transfer to ovarian cancer cells.
CC The modified adenovirus has an altered tropism, which allows the
CC adenovirus to be targeted to selected cell types. The recombinant
CC adenovirus can be used to provide gene therapy for individuals suffering
CC from cancer, cystic fibrosis and Duchenne's muscular dystrophy
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 5
AAY43233
ID AAY43233 standard; peptide; 9 AA.
XX
AC AAY43233;
XX
DT 13-JAN-2000 (first entry)
XX
DE RGD-containing peptide #12.
XX
KW Nucleic acid delivery vehicle; bifunctional complex; transgene; CFTR;
KW cell surface targeting; cell surface molecule binding region; integrin;
KW cystic fibrosis transmembrane regulator; alpha1-antitrypsin;
KW suicide gene; beta-glucocerebrosidase; cell transfection; cell infection;
KW RGD peptide.
XX
OS Synthetic.
XX
PN WO9940214-A2.
XX
PD 12-AUG-1999.
XX
PF 08-FEB-1999; 99WO-US002680.
XX
PR 09-FEB-1998; 98US-00020483.
PR 09-FEB-1998; 98US-0135092P.
PR 06-NOV-1998; 98US-0107471P.
XX
PA (GENZ) GENZYME CORP.
XX
PI O'riordan C, Romanczuk H, Wadsworth SC;
XX
DR WPI; 1999-610583/52.
XX
PT Nucleic acid delivery vehicles useful for transfecting and infecting a
PT target cell.
XX
PS Claim 22; Page 39; 118pp; English.
XX
CC This sequence represents a RGD-containing peptide that can be used in a
CC bifunctional complex used in the nucleic acid delivery vehicle (I) of the
CC invention. (I) is for transfecting and/or infecting a target cell, and
CC comprises a transgene and a bifunctional complex (B) that targets the
CC nucleic acid delivery vehicle to the cell surface. (B) comprises a
CC delivery vehicle binding portion, a cell surface molecule binding portion
CC (such as this sequence) and a linker connecting them. The delivery
CC vehicle can be specifically targeted to the cell via the binding to cell
CC surface molecules. (I) can be used to target cells, which express
CC integrins such as, HT-29 colon carcinoma cells, lymphocytes and
CC monocytes, blood platelets, SMC-90 human lung fibroblast, MG(63)
CC osteosarcoma cell line, vascular endothelial cells and melanoma cells.
CC (I) is useful for delivery of nucleic acids encoding CFTR (cystic
CC fibrosis transmembrane regulator), alpha1-antitrypsin, beta-
CC glucocerebrosidase and suicide genes. The construct increases the
CC efficiency of cellular uptake of (I). The constructs also enable the
CC transfection/infection of cells that are normally refractory to
CC transfection/infection by targeting cell receptors that are present on
CC such cells
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 6
AAW93626
ID AAW93626 standard; protein; 9 AA.
XX
AC AAW93626;
XX
DT 28-JUN-1999 (first entry)
XX
DE NGR receptor binding tumour homing peptide 5.
XX
KW Tumour homing peptide; tumour; diagnosis; endothelial cell;

KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
KW anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug;
KW prognosis; inflammation; regeneration; wounded tissue; targetting;
KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
KW occlusive thrombus.
XX
OS Synthetic.
XX
PN WO9913329-A1.
XX
PD 18-MAR-1999.
XX
PF 08-SEP-1998; 98WO-US018895.
XX
PR 10-SEP-1997; 97US-00926914.
PR 25-AUG-1998; 98US-00139802.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti E, Pasqualini R;
XX
DR WPI; 1999-215158/18.
XX
PT Identifying molecules that home to angiogenic vasculature used as targets
PT for anticancer agents.
XX
PS Claim 15; Page 7; 180pp; English.
XX
CC This invention describes novel peptides which home to angiogenic
CC vasculature, specifically of a tumour and which have anti-tumour, anti-
CC inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules
CC are identified by treating a purified NGR receptor with a test compound
CC and identifying compounds that bind specifically to the NGR receptor. The
CC peptides of the invention are inhibitors of angiogenesis and can be used
CC to produce conjugates for delivering agents to angiogenic vasculature,
CC particularly anticancer drugs or an imaging agent, for diagnosis or
CC prognosis. These conjugates may be directed to non-tumour angiogenic
CC vasculature, e.g. that present in inflammatory, regenerating or wounded
CC tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
CC or rheumatoid arthritis. The peptides provide specific targeting to
CC tumours, especially their supporting vasculature, since the NGR receptor
CC is exposed to the circulation only in angiogenic vasculature. Precise
CC targeting should reduce the systemic toxicity of anticancer drugs in the
CC conjugates. Complete killing of all target cells may not be essential
CC since partial denudation of endothelium may result in an occlusive
CC thrombus, and endothelial cells are unlikely to become resistant to
CC anticancer agents nor to lose the targeting receptor. AAW93622-W93809 and
CC AAW93843-44 are examples of tumour homing peptides used in the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 7
AAY48821
ID AAY48821 standard; peptide; 9 AA.
XX
AC AAY48821;
XX
DT 20-MAR-2003 (revised)
DT 10-DEC-1999 (first entry)
XX
DE Membrane dipeptidase-binding retina homing peptide #7.
XX
KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW membrane dipeptidase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9946284-A2.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US005284.
XX
PR 13-MAR-1998; 98US-00042107.
PR 26-FEB-1999; 99US-00258754.
XX
PA (BURN-) BURNHAM INST.
XX
PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX
DR WPI; 1999-571717/48.
XX
PT New peptides which selectively home to organs or tissues, used for, e.g.
PT identifying target ligands and for therapy of pathological conditions.
XX
PS Example 6; Page 149; 193pp; English.
XX
CC The present invention describes peptides that selectively home to a
CC tissue or organ. The peptides can be used for identifying an organ or
CC tissue, for identifying a target molecule expressed by an organ or tissue
CC or for treating an organ or tissue pathology, where the organ or tissue
CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
CC used in the exemplification of the present invention. (Updated on 20-MAR-
CC 2003 to correct PR field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 8
AAY54271
ID AAY54271 standard; peptide; 9 AA.
XX
AC AAY54271;
XX
DT 06-APR-2000 (first entry)
XX
DE Alpha Vbeta-3 binding peptide sequence.
XX
KW Envelope protein; mutant; retrovirus; surface protein shedding;
KW envelope protein stability; gene therapy; drug therapy; cancer;
KW adenosine deaminase deficiency; thalassemia; hemophilia; diabetes;
KW alpha-anti trypsin deficiency; brain disorder; neural disorder;
KW phenylketonuria; growth disorder; heart disease; immune disease.
XX
OS Unidentified.
XX
PN WO9960110-A2.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011155.
XX
PR 20-MAY-1998; 98US-0086149P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.

XX
PI Albritton LM, Zavorotinskaya T;
XX
DR WPI; 2000-116313/10.
XX
PT Novel isolated nucleic acid, useful for gene therapy.
XX
PS Example 10; Page 84; 190pp; English.
XX
CC The specification describes mutant retrovirus envelope proteins. The
CC envelope protein coding sequence can be mutated to encode a mutant
CC envelope protein with a substitution of one or more amino acids in at
CC least one motif of the retrovirus protein. The mutant protein fragment
CC allows for decreased shedding of the surface protein by suppressing
CC precursor cleavage and increase envelope stability and fusion of
CC retroviruses with cell membranes, while maintaining mutant envelope
CC protein incorporation into a virion, and viral titers of about two orders
CC of magnitude within that observed for wild-type retrovirus when the
CC protein or fragment is expressed on the surface of a retroviral particle.
CC The proteins have an increased ability to penetrate targets, typically
CC cells and a correspondingly increased ability to deliver nucleic acids or
CC drugs. The mutated nucleic acid is useful for gene and drug therapy,
CC especially as drug delivery vehicles. The retrovirus particles can be
CC utilized to transduce eukaryotic cells. The transduced cells are useful
CC in the treatment of cancer in a human. Other diseases contemplated for
CC treatment include adenosine deaminase deficiency (ADA), thalassemia,
CC hemophilia, diabetes, alpha-anti trypsin deficiency, brain and neural
CC disorders, phenylketonuria, growth disorders, heart diseases and immune
CC diseases. The present sequence was used in the course of the invention,
CC to quantitate targeted retroviral vector gene delivery in vivo
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 9
AAY44970
ID AAY44970 standard; protein; 9 AA.
XX
AC AAY44970;
XX
DT 23-MAY-2000 (first entry)
XX
DE RGD-4C targeting sequence for KDEL receptor inhibitor protein.
XX
KW KDEL receptor inhibitor; heat shock protein; immune response;
KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
KW melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
KW infectious disease; allergy; autoimmune disease.
XX
OS Unidentified.
XX
PN WO200006729-A1.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-US017147.
XX
PR 29-JUL-1998; 98US-00124671.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Rothman JE, Mayhew M, Hoe MH;
XX
DR WPI; 2000-195296/17.
XX
PT Inhibitors of the KDEL receptor which comprises an oligomerization domain
PT useful for promoting secretion of proteins which are normally retained
PT within the cell.
XX
PS Disclosure; Page 17; 87pp; English.
XX
CC The patent discloses the use of KDEL receptor inhibitor to promote
CC secretion of proteins that are normally retained within the cell such as
CC heat shock proteins by inhibiting KDEL receptor-mediated return of
CC protein complexes to endoplasmic reticulum. This makes the secreted heat
CC shock proteins more accessible to the immune system and improves immune
CC response to a target antigen. The inhibitor protein comprises several
CC subunits where each subunit comprises an oligomerisation domain and has
CC at its carboxy terminus a region which binds to a KDEL receptor. The
CC target antigen may be associated with diseases including neoplasia such
CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
CC astromytoma, with defective tumour suppressor genes, oncogenes,
CC infectious diseases, allergy or autoimmune diseases. The present sequence
CC is a targeting peptide termed RGD-4C. This may be incorporated into the
CC amino terminal region of a KDEL receptor inhibitor protein downstream
CC from a cleavably removed sequence to improve its activity or alter its
CC immunogenicity
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 10
AAB17928
ID AAB17928 standard; peptide; 9 AA.
XX
AC AAB17928;
XX
DT 31-OCT-2000 (first entry)
XX
DE TPO-mimetic peptide sequence SEQ ID NO:1032.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Disclosure; Page 559; 608pp; English.

XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 11
AAB17964
ID AAB17964 standard; peptide; 9 AA.
XX
AC AAB17964;
XX
DT 31-OCT-2000 (first entry)
XX
DE Integrin-binding peptide sequence SEQ ID NO:1076.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 591; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 12
AAB17346
ID AAB17346 standard; peptide; 9 AA.
XX
AC AAB17346;
XX
DT 31-OCT-2000 (first entry)
XX
DE Integrin-binding peptide sequence SEQ ID NO:450.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Claim 39; Page 354; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 13
AAY90211
ID AAY90211 standard; peptide; 9 AA.
XX
AC AAY90211;
XX
DT 06-AUG-2003 (revised)
DT 21-SEP-2000 (first entry)
XX
DE Alphav integrin targeting peptide #1.
XX
KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;
KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
KW smooth muscle cell proliferation inhibitor; coronary artery disease;
KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
KW thrombosis; diabetes; tropism-modified virus.
XX
OS Synthetic.
XX
PN WO200012738-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-IB001524.
XX
PR 27-AUG-1998; 98US-0098028P.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;
XX
DR WPI; 2000-256653/22.
XX
PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
PT vectors having modified hexon HRV5 and HI loops and modified fiber
PT proteins useful for targeted gene therapy to treat cancer or restenosis.
XX
PS Example 5; Page 53; 128pp; English.
XX
CC This sequence represents a alphav integrin targeting peptide. The
CC invention relates to an adenovirus from which at least a part of the
CC hexon HVR5 or HI loop is replaced with a binding peptide, or targeting
CC sequence, flanked by connecting amino acid spacers, to functionally
CC display its binding specificity at the capsid surface. The invention also
CC relates to a recombinant adenovirus vector where a binding peptide, or
CC targeting sequence, is connected to the C-terminus of the fiber by a
CC connecting spacer, or linker, so as to functionally display its binding
CC specificity at the capsid surface. The adenovirus or recombinant
CC adenovirus vector can be used to preferentially express a gene in a
CC target cell, especially a cell that expresses a UPAR. The targeted
CC adenovirus vector preferably comprises a heterologous gene encoding a
CC gene for treatment of a tumour or restenosis. The targeted adenovirus
CC vector is useful for gene therapy treatment of a disease, and for
CC manufacturing a medicine used in gene therapy treatment of a disease. The
CC viruses can also be used to inhibit smooth muscle cell proliferation, to
CC treat peripheral artery diseases, coronary artery diseases, obesity,
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
CC thrombosis, and diabetes. The viruses are particularly targeted against a
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
CC are tropism-modified without adversely impacting productivity of the
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 14
AAO22875
ID AAO22875 standard; peptide; 9 AA.
XX
AC AAO22875;
XX
DT 30-JAN-2003 (first entry)
XX
DE Angiogenic treatment compound related synthetic peptide #75.
XX
KW Cyclic; cytostatic; antitumour; targeting moiety; chelator; peptide;
KW peptidomimetic; angiogenesis; metallopharmaceutical; new blood vessel;
KW rheumatoid arthritis; cancer; cancer planar; SPECT gamma scintigraphy;
KW positron emission; X-ray computed tomography; magnetic resonance imaging;
KW synthetic cyclic peptide.
XX
OS Synthetic.
XX
PN WO9958162-A2.
XX
PD 18-NOV-1999.
XX
PF 29-MAR-1999; 99WO-US006826.
XX
PR 31-MAR-1998; 98US-0080150P.
PR 18-DEC-1998; 98US-0112715P.
XX
PA (DUPO) DU PONT PHARM CO.
XX
PI Rajopadhye M, Edwards DS, Harris TD, Heminway SJ, Liu S;
PI Singh PR;
XX
DR WPI; 2000-105546/09.
XX
PT Novel compound for diagnosis and treatment of cancer.
XX
PS Disclosure; Page 62; 213pp; English.
XX
CC The invention relates to compounds comprising targeting moiety which is
CC bound to a chelator. The targeting moiety is a peptide or peptidomimetic
CC which binds to a receptor and is upregulated during angiogenesis. The
CC compound has 0-1 linking groups between targeting moiety and the
CC chelator. The metallopharmaceutical composition is used in treating
CC rheumatoid arthritis or cancer by imaging the formation of new blood
CC vessels, imaging cancer planar or SPECT gamma scintigraphy, positron
CC emission or X-ray computed tomography or with magnetic resonance imaging.
CC This sequence represents a synthetic cyclic peptide relating to the novel

```
CC   compounds of the invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 15
AAB21701
ID   AAB21701 standard; peptide; 9 AA.
XX
AC   AAB21701;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human breast tumour homing peptide #1.
XX
KW   Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW   breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
XX
OS   Homo sapiens.
XX
PN   WO200042973-A2.
XX
PD   27-JUL-2000.
XX
PF   21-JAN-2000; 2000WO-US001602.
XX
PR   22-JAN-1999;   99US-00235902.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Ellerby HM,  Bredesen DE,  Pasqualini R,  Ruoslahti EI;
XX
DR   WPI; 2000-499174/44.
XX
PT   Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT   selectively homes to a mammalian cell type or tissue linked to an
PT   antimicrobial peptide, useful for the treatment of prostate cancer.
XX
PS   Claim 12; Page 105; 118pp; English.
XX
CC   The present invention relates to homing pro-apoptotic conjugates,
CC   comprising of a tumour homing molecule that selectively homes to a
CC   mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC   homing pro-apoptotic conjugates are selectively internalised by the
CC   mammalian cell type or tissue and exhibits high toxicity, especially to
CC   angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC   toxicity when not linked to the tumor homing molecule. The conjugates are
CC   useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC   prostate cancer or melanoma. The present sequence is a homing peptide
CC   isolated in the present invention, which can be conjugated to an
CC   antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC   present invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 16
AAB20271
ID   AAB20271 standard; peptide; 9 AA.
XX
AC   AAB20271;
XX
DT   14-MAY-2001  (first entry)
XX
DE   Peptide that specifically targets tumour blood vessels.
XX
KW   Tumour; breast carcinoma; Karposi's sarcoma; melanoma;
KW   fiberless radiative effector; therapy; imaging.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4. .6
FT                   /note= "RGD motif"
XX
PN   WO200108660-A2.
XX
PD   08-FEB-2001.
XX
PF   26-JUL-2000; 2000WO-US020292.
XX
PR   02-AUG-1999;   99US-00366314.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Philbert MA,  Tjalkens R,  Aylott JW,  Clark HA,  Monson EE;
PI   Kopelman R;
XX
DR   WPI; 2001-182851/18.
XX
PT   Composition for destroying or inhibiting growth of tumor cells and for
PT   imaging tumors or other biological targets, has molecular recognition
PT   element attached to fiberless radiative effector having a toxic agent.
XX
PS   Disclosure; Page 35; 95pp; English.
XX
CC   The present sequence is that of a peptide that specifically binds to
CC   tumour blood vessels. It includes an RGD motif. The peptide, and
CC   conjugates containing it, selectively binds to various tumours, including
CC   breast carcinomas, Karposi's sarcoma and melanoma. The peptide can be
CC   used as the molecular recognition element of novel fiberless radiative
CC   effectors (FREs) of the invention. The invention is related to cell or
CC   pathogen destruction via FREs that encapsulate a radical generator. The
CC   FREs include a polymer matrix, a photodynamic or radiodynamic dye which
CC   produces free radicals upon stimulation, cloaking material, and at least
CC   1 molecular recognition element for targeting to a biological target,
CC   e.g. the present peptide. They are useful in various in vitro and in vivo
CC   procedures, destroying or inhibiting the growth of biological targets
CC   (pathogens, macromolecules, tumour cells in culture or in the body), in
CC   therapies including chemotherapy, radiation therapy, antibiotic and
CC   vaccine therapy
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 17
AAB50242
ID   AAB50242 standard; peptide; 9 AA.
XX
AC   AAB50242;
XX
DT   13-MAR-2001  (first entry)
```

XX
DE Enhanced infectivity adenoviral vector fibre replacement ligand.
XX
KW Adenoviral vector; gene therapy; infectability;
KW tumour-specific replication.
XX
OS Unidentified.
XX
PN WO200067576-A1.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013114.
XX
PR 12-MAY-1999; 99US-0133634P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Curiel DT, Krasnykh VN, Alemany R, Dmitriev I;
XX
DR WPI; 2001-122702/13.
XX
PT New infectivity-enhanced, conditionally-replicative adenovirus containing
PT a modified wild type adenoviral fiber, useful for cancer therapy.
XX
PS Claim 8; Page 70; 104pp; English.
XX
CC The present invention provides an adenoviral vector with an enhanced
CC ability to infect tumour cells and which is conditionally replicative,
CC enabling replication in only one cell type. This can be used in the gene
CC therapy treatment of cancers
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 18
AAB97086
ID AAB97086 standard; peptide; 9 AA.
XX
AC AAB97086;
XX
DT 02-AUG-2001 (first entry)
XX
DE Integrin-binding peptide #4.
XX
KW Integrin; avB3; avB5; analgesic; cytostatic; macrocyclic chelant;
KW metal chelate formation; metalloradiopharmaceutical;
KW magnetic resonance imaging; MRI; disease diagnosis;
KW systemic radiotherapy; bone pain; bone cancer; antagonist.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "The amino group of the residue at position 1
FT forms a peptide bond with the carboxy group of the
FT residue at position 9 to form a cyclic molecule"
FT Modified-site 9
FT /note= "The amino group of the residue at position 1
FT forms a peptide bond with the carboxy group of the
FT residue at position 9 to form a cyclic molecule"
XX
PN WO200119838-A1.
XX
PD 22-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024482.
XX
PR 13-SEP-1999; 99US-0153512P.
XX
PA (DUPO) DU PONT PHARM CO.
XX
PI Liu S;
XX
DR WPI; 2001-389600/41.
XX
PT New nitrogen containing macrocyclic chelant compounds used in metal
PT chelates for e.g. X-ray imaging and for attaching diagnostic and
PT therapeutic isotopes to biologically active targeting molecules.
XX
PS Disclosure; Page 72; 121pp; English.
XX
CC The present sequence is provided in a specification relating to novel
CC nitrogen containing macrocyclic chelant compounds. The compounds are used
CC for forming metal chelates used as diagnostic or therapeutic
CC metalloradiopharmaceuticals, or magnetic resonance imaging (MRI) contrast
CC agents. They are also used for attaching metal ions to bio-directing
CC groups including proteins, peptides, peptidomimetics and non peptides
CC that bind in vivo to a receptor or enzyme that is expressed or up-
CC regulated at a site or in a disease state. The metallopharmaceuticals are
CC used in disease diagnosis by MRI or in treating disease by systemic
CC radiotherapy. Radiolanthide chelates with phosphonomethyl and optionally
CC carboxymethyl groups on the four N atoms can be used for treating bone
CC pain and bone metastases. The macrocyclic chelants rapidly form stable
CC metal chelates. The present sequence binds with high affinity to the
CC integrins avB3 and avB5
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 19
AAE06279
ID AAE06279 standard; peptide; 9 AA.
XX
AC AAE06279;
XX
DT 25-SEP-2001 (first entry)
XX
DE Tumour homing peptide used for homing pro-apoptotic conjugates.
XX
KW Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
KW antimicrobial peptide; prostate cancer; tumour homing molecule;
KW cytostatic; RGD motif.
XX
OS Synthetic.
XX
PN WO200153342-A1.
XX
PD 26-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001362.
XX
PR 21-JAN-2000; 2000US-00489582.
XX
PA (BURN-) BURNHAM INST.
XX
PI Ruoslahti EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
XX
DR WPI; 2001-451901/48.
XX

PT Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
PT prostate cancer, comprises a prostate-homing peptide linked to an
PT antimicrobial peptide.
XX
PS Example 3B; Page 84; 176pp; English.
XX
CC The patent discloses novel chimeric prostate-homing pro-apoptotic peptide
CC which comprises a prostate-homing peptide linked to an antimicrobial
CC peptide, where the chimeric peptide is selectively internalised by and
CC exhibits high toxicity to prostate tissue and where the antimicrobial
CC peptide has low mammalian cell toxicity when not linked to prostate-
CC homing peptide. The chimeric peptide is used to direct an antimicrobial
CC peptide in vivo to a prostate cancer, to induce selective toxicity in
CC vivo in a prostate cancer, and to treat a patient with prostate cancer.
CC The present peptide sequence is a tumour homing molecule containing a RGD
CC motif. This sequence is useful in the homing of pro-apoptotic conjugates
CC of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 20
AAE11044
ID AAE11044 standard; peptide; 9 AA.
XX
AC AAE11044;
XX
DT 18-DEC-2001 (first entry)
XX
DE RGD-containing peptide.
XX
KW Tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
KW melanoma.
XX
OS Unidentified.
XX
PN US6284236-B1.
XX
PD 04-SEP-2001.
XX
PF 26-MAY-1999; 99US-00320424.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
PR 25-JUN-1996; 96US-00670354.
PR 26-MAR-1998; 98US-00048641.
PR 10-NOV-1998; 98US-00190046.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Wiley SR, Goodwin RG;
XX
DR WPI; 2001-595463/67.
XX
PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
PT for treating viral infections (e.g. bovine viral diarrhea or human
PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX
PS Disclosure; Col 11; 41pp; English.
XX
CC The invention relates to a cytokine designated as tumour necrosis factor
CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
CC of certain target cells, including cancer cells and virally infected
CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
CC treating viral infections (e.g. bovine viral diarrhoea or human
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
CC melanoma), as a research reagent useful in studying apoptosis including
CC the regulation of programmed cell death. TRAIL DNA sequences may be
CC employed in developing a gene therapy approach to treating disorders
CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is a RGD-containing peptide that
CC binds an integrin associated with tumour. This sequence is used to
CC construct a fusion protein comprising TRAIL protein
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 21
AAU98837
ID AAU98837 standard; peptide; 9 AA.
XX
AC AAU98837;
XX
DT 22-AUG-2002 (first entry)
XX
DE Tumour homing peptide RGD-4C.
XX
KW Targeting peptide; cancer; tumour targeting; cytostatic; anti-HIV;
KW immunostimulant; immunogen; cancer; human immunodeficiency virus; HIV;
KW vector delivery.
XX
OS Synthetic.
XX
PN WO200220724-A2.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US028045.
XX
PR 08-SEP-2000; 2000US-0231266P.
PR 17-JAN-2001; 2001US-00765101.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR WPI; 2002-489672/52.
XX
PT Modulation of immune system response comprises administration of
PT targeting peptide attached to immunogen.
XX
PS Disclosure; Page 11; 86pp; English.
XX
CC This invention relates to a method for modulating the immune system
CC response comprising administration of a lymph node targeting peptide
CC attached to an immunogen. The invention also comprises a bispecific
CC compound comprising the sequences Cys-Ala-Tyr or Ser-Cys-Ala-Arg, a
CC bispecific compound comprising a targeting peptide attached to a vector
CC binding moiety and a method for targeting a vector to an organ or tissue
CC comprising administering the vector and a complex comprising a targeting
CC peptide and a binding moiety. The peptides of the invention may have
CC cytostatic, anti-HIV or immunostimulant activities. The method of the
CC invention is useful for increasing the immune response to an immunogen,
CC especially a cancer cell or human immunodeficiency virus (HIV). The
CC method is useful for the selective delivery of gene therapy vectors. The
CC present sequence represents an tumour homing peptide RGD-4C used in the
CC method of the invention

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 22
ABG35079
ID ABG35079 standard; peptide; 9 AA.
XX
AC ABG35079;
XX
DT 15-JUL-2002 (first entry)
XX
DE RGD-4C-beta gal phage transduction inhibitor peptide.
XX
KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
KW inflammatory disease; arthritis; atherosclerosis; cancer;
KW autoimmune disease; bacterial infection; viral infection.
XX
OS Synthetic.
XX
PN WO200220722-A2.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US027702.
XX
PR 08-SEP-2000; 2000US-0231266P.
PR 17-JAN-2001; 2001US-00765101.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR WPI; 2002-383050/41.
XX
PT Identifying targeting peptides useful for treating e.g. diabetes
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
PT comprises exposing a sample to a phage display library and recovering
PT phage bound to the sample.
XX
PS Disclosure; Page 262; 298pp; English.
XX
CC This invention relates to a novel method for identifying disease
CC targeting peptides. The method comprises exposing a sample from an organ,
CC tissue or cell type of interest, to a phage display library and
CC recovering phage bound to the sample (the phage expresses targeting
CC peptides). The peptides identified by the method of the invention may
CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
CC activities. The methods and composition are useful for identifying
CC targeting peptides and one or more receptors for a targeting peptide. The
CC targeting peptides are used for selective delivery of therapeutic agents,
CC including gene therapy vectors and fusion proteins, to specific organs,
CC tissues, or cell types in subject. The targeting peptide may also be used
CC for treating diseases such as diabetes mellitus, inflammatory diseases,
CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
CC viral infections and Hodgkin's disease. The present sequence represents a
CC targeting peptide of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 23
AAU81110
ID AAU81110 standard; peptide; 9 AA.
XX
AC AAU81110;
XX
DT 09-APR-2002 (first entry)
XX
DE Integrin-antagonist peptide #17.
XX
KW IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW echistatin; integrin; selectin; vinculin; platelet aggregation;
KW angiogenesis; tumour; inflammation; autoimmune disease;
KW rheumatoid arthritis; osteoporosis.
XX
OS Synthetic.
XX
PN WO200181377-A2.
XX
PD 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-US013069.
XX
PR 21-APR-2000; 2000US-0198919P.
PR 03-MAY-2000; 2000US-0201394P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Kohno T, Lacey DL, Boone TC;
XX
DR WPI; 2002-062025/08.
XX
PT Composition comprising integrin or adhesion antagonistic peptide and
PT vehicle, useful for treating or preventing platelet aggregation, has a
PT longer half-life than free peptide.
XX
PS Claim 11; Page 19; 68pp; English.
XX
CC The invention relates to a composition comprising an integrin/adhesion
CC antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
CC based on laminin or saw-scaled viper echistatin and target integrin,
CC selectin or vinculin.Also included are compounds of formula (Ia) and
CC their multimers (X^1)_a-P^1-(X^2)_b where; F^1 = Fc domain; X^1 and X^2 =
CC -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2, (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-
CC P^3 or (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4; P^1-P^4 = same or
CC different (I); L^1-L^4 = same or different linkers; a-f = 0 or 1,
CC provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC an expression vector containing the nucleic acid, host cells containing
CC the vector, producing a pharmaceutically active compound (B) by
CC covalently linking at least one Fc domain to at least one amino acid
CC sequence of a selected randomized (I) and any of six laminin-related
CC peptides (Ib). The compositions are used prophylactically and
CC therapeutically in the same way as (I), e.g. to inhibit platelet
CC aggregation or angiogenesis (tumours), or to treat inflammation and
CC autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC domain) to (I) increases the half-life (free (I) are normally degraded
CC very quickly in vivo). The present sequence is an antagonist peptide of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9
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RESULT 24
AAU81134
ID   AAU81134 standard; peptide; 9 AA.
XX
AC   AAU81134;
XX
DT   09-APR-2002  (first entry)
XX
DE   Integrin-antagonist peptide #41.
XX
KW   IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW   immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW   echistatin; integrin; selectin; vinculin; platelet aggregation;
KW   angiogenesis; tumour; inflammation; autoimmune disease;
KW   rheumatoid arthritis; osteoporosis.
XX
OS   Synthetic.
XX
PN   WO200181377-A2.
XX
PD   01-NOV-2001.
XX
PF   23-APR-2001; 2001WO-US013069.
XX
PR   21-APR-2000; 2000US-0198919P.
PR   03-MAY-2000; 2000US-0201394P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Kohno T,  Lacey DL,  Boone TC;
XX
DR   WPI; 2002-062025/08.
XX
PT   Composition comprising integrin or adhesion antagonistic peptide and
PT   vehicle, useful for treating or preventing platelet aggregation, has a
PT   longer half-life than free peptide.
XX
PS   Claim 11; Page 19; 68pp; English.
XX
CC   The invention relates to a composition comprising an integrin/adhesion
CC   antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
CC   based on laminin or saw-scaled viper echistatin and target integrin,
CC   selectin or vinculin.Also included are compounds of formula (Ia) and
CC   their multimers (X^1)_a-F^1-(X^2)_b where; F^1 = Fc domain; X^1 and X^2 =
CC   -(L^1)_c-P^1, (L^1)_c-P^1-(L^2)_d-P^2, (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-
CC   P^3 or (L^1)_c-P^1-(L^2)_d-P^2-(L^3)_e-P^3-(L^4)_f-P^4; P^1-P^4 = same or
CC   different (I); L^1-L^4 = same or different linkers; a-f = 0 or 1,
CC   provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC   an expression vector containing the nucleic acid, host cells containing
CC   the vector, producing a pharmaceutically active compound (B) by
CC   covalently linking at least one Fc domain to at least one amino acid
CC   sequence of a selected randomized (I) and any of six laminin-related
CC   peptides (Ib). The compositions are used prophylactically and
CC   therapeutically in the same way as (I), e.g. to inhibit platelet
CC   aggregation or angiogenesis (tumours), or to treat inflammation and
CC   autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC   of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC   domain) to (I) increases the half-life (free (I) are normally degraded
CC   very quickly in vivo). The present sequence is an antagonist peptide of
CC   the invention
XX
SQ   Sequence 9 AA;
```

```
  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9
```

```
RESULT 25
ABP54051
ID   ABP54051 standard; peptide; 9 AA.
XX
AC   ABP54051;
XX
DT   13-JAN-2003  (first entry)
XX
DE   Alpha-v-beta-3 and alpha-v-beta-5 binding peptide #1.
XX
KW   Radiopharmaceutical; radioisotope; imaging; cardiac perfusion;
KW   vitronectin receptor; angiogenesis; organ perfusion; plaque; perfusion.
XX
OS   Synthetic.
XX
PN   WO200255111-A2.
XX
PD   18-JUL-2002.
XX
PF   26-NOV-2001; 2001WO-US044155.
XX
PR   27-NOV-2000; 2000US-0253324P.
XX
PA   (BRIS-) BRISTOL MYERS SQUIBB MEDICAL IMAGING INC.
XX
PI   Carpenter AP;
XX
DR   WPI; 2002-740676/80.
XX
PT   Concurrent imaging, useful for localization of sites of angiogenesis,
PT   comprises use of a vitronectin receptor targeted imaging agent and a
PT   perfusion imaging agent.
XX
PS   Disclosure; Page 85; 272pp; English.
XX
CC   The present invention describes a method for the concurrent imaging in a
CC   mammal (I). The method comprises: (A) administering a vitronectin
CC   receptor targeted and a perfusion imaging agent; (B) detecting the
CC   vitronectin receptor targeted imaging agent bound at the vitronectin
CC   receptor and perfusion imaging agent; and (C) forming an image from the
CC   detection of the vitronectin targeted imaging and perfusion imaging
CC   agent. Also described is a kit (II), comprising a vitronectin receptor
CC   targeted imaging agent and perfusion imaging agent. (I) is for use in
CC   concurrent site of angiogenesis and organ perfusion, for diagnosing and
CC   localisation of site of vulnerable plaque and perfusion abnormalities.
CC   The vitronectin targeted imaging agent and a perfusion imaging agent have
CC   spectrally separable approx.g-emission energies. The images are displayed
CC   side-by side or overlapped to facilitate interpretation of the
CC   localisation of the vitronectin targeted imaging in the body, relative to
CC   the distribution of the perfusion agent in the body. The perfusion
CC   imaging agents are spectrally separable by pulse-height analysis. The
CC   difference in approx.g emission spectral energies of the vitronectin
CC   antagonist diagnostic metallopharmaceutical and the perfusion agent is
CC   less than 10 Kev. The present sequence represents an alpha-v-beta-3 and
CC   alpha-v-beta-5 binding peptide, which is given in the exemplification of
CC   the present invention
XX
SQ   Sequence 9 AA;
```

```
  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9
```

RESULT 26
ABB72945
ID ABB72945 standard; peptide; 9 AA.
XX
AC ABB72945;
XX
DT 05-APR-2002 (first entry)
XX
DE Integrin binding peptide SEQ ID NO:450.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 47; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 27
ABB72961
ID ABB72961 standard; peptide; 9 AA.
XX
AC ABB72961;
XX
DT 05-APR-2002 (first entry)
XX
DE Integrin binding peptide SEQ ID NO:1076.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 47; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777

```
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 28
ABJ04359
ID   ABJ04359 standard; peptide; 9 AA.
XX
AC   ABJ04359;
XX
DT   24-OCT-2002  (first entry)
XX
DE   BRASIL method-related peptide 3.
XX
KW   BRASIL; targeting peptide; bacterial infection;
KW   Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
KW   inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
KW   viral infection; cardiovascular disease; degenerative disease.
XX
OS   Unidentified.
XX
PN   WO200220822-A2.
XX
PD   14-MAR-2002.
XX
PF   07-SEP-2001; 2001WO-US028124.
XX
PR   08-SEP-2000; 2000US-0231266P.
PR   17-JAN-2001; 2001US-00765101.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Arap W,  Pasqualini R;
XX
DR   WPI; 2002-404697/43.
XX
PT   Identification of targeting peptides that can be used to treat diseases
PT   e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT   of Selective Ligands) method comprises a single differential
PT   centrifugation step.
XX
PS   Example 1; Page 57; 167pp; English.
XX
CC   The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
CC   of Selective Interactive Ligands) to obtain a targeting peptide. The
CC   BRASIL method of the invention involves: exposing a target to a phage
CC   display library in a first phase; exposing the first phase to a second
CC   phase; and separating the phage bound to the target from unbound phage.
CC   The BRASIL method of the invention allows cell phages to be separated
CC   from the remaining unbound phage in a single differential centrifugation
CC   step. When compared to conventional cell panning methods, the BRASIL
CC   method shows a significant increase in recovery of specific phage and a
CC   substantial decrease in background. The BRASIL method is useful for
CC   identifying targeting peptides. The targeting peptides identified by the
CC   method of the invention are useful for treating disease states, such as:
CC   diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
CC   disease; bacterial infection; viral infection; cardiovascular disease and
CC   degenerative disease. The present amino acid sequence represents a
CC   peptide that was used in the method of the invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 29
ABB08066
ID   ABB08066 standard; peptide; 9 AA.
XX
AC   ABB08066;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Cyclic RGD (cRGD) targeting ligand domain.
XX
KW   Targeting molecule; adenoviral receptor domain; trimerisation; cancer;
KW   coxsackie-adenovirus receptor; CAR; transmembrane protein; cytostatic;
KW   hepatotropic; virucide; gene therapy; RGD; cRGD; cyclic.
XX
OS   Homo sapiens.
XX
PN   WO200229072-A2.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-EP011514.
XX
PR   06-OCT-2000; 2000US-00684552.
PR   06-OCT-2000; 2000US-0327562P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Kim JG,  Smith T,  Stevenson SC,  Kaleko M;
XX
DR   WPI; 2002-471317/50.
XX
PT   A targeting molecule for use in forming complexes to treat cancer, such
PT   as adenocarcinoma of the prostate, comprises a soluble adenoviral
PT   receptor domain, a trimerization domain and a targeting ligand domain.
XX
PS   Example 2; Page 32; 75pp; English.
XX
CC   The invention relates to a targeting molecule that comprises a soluble
CC   adenoviral receptor domain, a trimerisation domain and a targeting ligand
CC   domain. The targeting molecules are used for targeting an adenoviral
CC   particle to a cell expressing a cell surface molecule. The method
CC   involves contacting the adenoviral particle with the targeting molecule
CC   to form a complex, and contacting the cell with the complex, and in
CC   delivering a heterologous gene selectively to a cell. The complex is used
CC   for preparing a medicament for treatment of disease in a human mammal,
CC   such as cancer, preferably, adenocarcinoma of the prostate, by gene
CC   therapy. The present sequence represents a cyclic RGD (cRGD) targeting
CC   ligand domain, used in the targeting molecule of the invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 30
ABG70729
ID   ABG70729 standard; peptide; 9 AA.
XX
```

AC ABG70729;
XX
DT 27-NOV-2002 (first entry)
XX
DE avB3 binding cyclic peptide #4.
XX
KW Macrocyclic chelant; pathological process; angiogenic neovasculature;
KW contrast agent; X-ray; CT; computerised tomography; magnetic resonance;
KW radiopharmaceutical; cardiovascular disorder; infectious disease; cancer;
KW imaging; hypoxia; apoptosis; cardiac ischaemia; thrombosis; infection;
KW inflammation; restenosis; atherosclerosis; diabetic retinopathy;
KW macular degeneration; wound healing; reperfusion injury; cytostatic;
KW heavy metal detoxification; avB3; cyclic; circular.
XX
OS Synthetic.
XX
PN US2002098149-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033765.
XX
PR 09-JAN-2001; 2001US-0260500P.
XX
PA (LIUS/) LIU S.
XX
PI Liu S;
XX
DR WPI; 2002-706013/76.
XX
PT New macrocyclic chelants and metal chelates useful for treating e.g.
PT pathological processes involving angiogenic neovasculature and as
PT contrast agents.
XX
PS Disclosure; Page 11; 21pp; English.
XX
CC The present invention relates to new macrocyclic chelants. The invention
CC can be used for treating pathological processes involving angiogenic
CC neovasculature and as contrast agents in X-ray, CT (computerised
CC tomography), magnetic resonance and radiopharmaceuticals for the
CC diagnosis of cardiovascular disorders, infectious disease and cancer, and
CC for imaging hypoxia, apoptosis, cardiac ischaemia, thrombosis, infection,
CC inflammation, restenosis, atherosclerosis, diabetic retinopathy, macular
CC degeneration, wound healing and reperfusion injury. The invention is also
CC useful for heavy metal detoxification. The present amino acid sequence
CC represents a cyclic peptide that was used in the methods of the invention
CC to bind to avB3
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 31
ABB76442
ID ABB76442 standard; peptide; 9 AA.
XX
AC ABB76442;
XX
DT 02-SEP-2002 (first entry)
XX
DE RGD-4C Peptide with integrin binding affinity.
XX
KW Integrin; adenovirus; vector; cancer; tumour; gene therapy.
XX
OS Synthetic.
XX
PN US2002058045-A1.
XX
PD 16-MAY-2002.
XX
PF 01-MAY-2001; 2001US-00845160.
XX
PR 31-MAY-2000; 2000JP-00161577.
PR 27-APR-2001; 2001JP-00131688.
XX
PA (NAHE-) NAT INST HEALTH SCI.
XX
PI Mizuguchi H, Hayakawa T;
XX
DR WPI; 2002-499507/53.
DR N-PSDB; ABN83749.
XX
PT A method for constructing a fiber-mutant adenovirus vector in which a
PT foreign peptide is introduced by a simple system into the fiber HI loop-
PT coding gene of adenovirus providing a more effective means of introducing
PT foreign peptides.
XX
PS Example 1; Page 4; 13pp; English.
XX
CC The present sequence is that of an RGD-4C peptide having binding affinity
CC to cell surface integrins. DNA encoding a foreign peptide, such as the
CC present sequence, may be introduced into a fibre HI loop-coding gene
CC sequence using a method of the invention for construction of fibre-mutant
CC adenovirus vectors. The fibre HI loop comprises amino acids 537-549 of a
CC fibre molecule. Insertion of a foreign peptide into this region does not
CC affect the formation of trimers by the fibre molecules. A claimed method
CC for constructing a fibre-mutant adenovirus vector comprises inserting a
CC unique restriction enzyme recognition sequence, especially Csp45I and/or
CC ClaI, into the fibre HI loop-encoding gene, and introducing a foreign
CC peptide-encoding DNA into the gene sequence. The peptide preferably
CC includes the tripeptide Arg-Gly-Asp (RGD) or Asn-Gly-Arg (NGR) and has
CC tropism for tumour vascular endothelial cells. Selection of RGD-4C as the
CC foreign peptide can improve the efficiency of gene introduction not only
CC to adenovirus-sensitive cells but also to e.g. CHO cells, respiratory
CC epidermic cells, smooth muscle cells, vascular endothelial cells, T-
CC cells, macrophages, haematopoietic stem cells, dendritic cells and cancer
CC cells which are CAR-negative but which express integrins on their
CC surfaces, e.g. human glioma LN444 cells. A synthetic oligonucleotide
CC encoding the peptide and including Csp45I and ClaI restriction sites can
CC be ligated directly into the HI loop-coding gene sequence digested with
CC the corresponding restriction enzymes. The fiber-mutant adenovirus vector
CC has high gene transfer efficiency
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 32
AAE17983
ID AAE17983 standard; peptide; 9 AA.
XX
AC AAE17983;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human ligand #3 attached to an adenoviral vector.
XX
KW Human; adenoviral coat protein; non-native ligand; cell-surface receptor;
KW therapy; anti-tumour agent; tumour necrosis factor; cancer; brain; lung;
KW ovary; breast; prostate; alphavbeta3 integrin.
XX
OS Homo sapiens.

XX
PN WO200192549-A2.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US017391.
XX
PR 31-MAY-2000; 2000US-0208451P.
PR 02-AUG-2000; 2000US-00631191.
XX
PA (GENV-) GENVEC INC.
XX
PI Wickham TJ, Kovesdi I, Roelvink PW, Einfeld D, Brough DE;
PI Lizonova A;
XX
DR WPI; 2002-147620/19.
XX
PT Adenoviral coat protein which permits production of adenoviral vectors
PT that bind and infect host cells not naturally infected by adenovirus,
PT comprises various non-native ligands.
XX
PS Claim 4; Page 40; 45pp; English.
XX
CC The invention relates to adenoviral coat proteins comprising various non-
CC native ligands. The invention provides a method of controlled gene
CC expression utilising selectively replication competence and also a method
CC and a composition for targetting an adenoviral vector. A system
CC comprising a cell having a non-native cell-surface receptor, and a virus
CC having a non-native ligand which binds the non-native cell-surface
CC receptor of the cell is useful for propagating a virus and also for
CC assaying gene function. The system is also useful for isolating a nucleic
CC acid encoding a product comprising a desired property. Further the system
CC is useful for identifying functionally related coding sequences.
CC Adenoviral vector comprising a non-native nucleic acid encoding a
CC therapeutic agent such as anti-tumour agent, preferably tumour necrosis
CC factor and a second non-native nucleic acid encoding an agent that
CC facilitates imaging and a targetting agent is useful for treating an
CC animal. The therapeutic agent can be used to treat cancer of the brain,
CC lung, ovary, breast and prostate. The present sequence is human non-
CC native ligand specific for alphavbeta3 integrin, attached to an
CC adenoviral vector
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 33
ABB78354
ID ABB78354 standard; peptide; 9 AA.
XX
AC ABB78354;
XX
DT 16-DEC-2002 (first entry)
XX
DE Amino acid sequence of a peptide ligand.
XX
KW Tetraether lipid derivative; liposome; lipid aggregate;
KW in vitro transfection; gene therapy; packaging; peptide ligand; circular.
XX
OS Unidentified.
XX
PN DE10065561-A1.
XX
PD 11-JUL-2002.
XX
PF 28-DEC-2000; 2000DE-01065561.
XX
PR 28-DEC-2000; 2000DE-01065561.
XX
PA (BERN-) BERNINA BIOSYSTEMS GMBH.
XX
PI Kuehl C, Tewes B, Hagen M, Gropp F, Littger R, Marx U;
XX
DR WPI; 2002-675953/73.
XX
PT New tetraether lipid derivative, useful e.g. for preparing liposomes and
PT lipid aggregates for gene therapy or in vitro transfection.
XX
PS Disclosure; Page 12; 44pp; German.
XX
CC The invention describes tetraether lipid derivatives, of a formula given
CC in the specification. Liposomes, or lipid aggregates, that contain one or
CC more of these lipid derivatives are useful for in vitro transfection of
CC eukaryotic cells; for gene therapy and for packaging active ingredients
CC for oral, (par)enteral or topical delivery. The lipid derivatives are
CC also used to coat surfaces, e.g. of metal or plastic, such as stents and
CC implants, and, where the resulting monolayers also include hydrophobic
CC active ingredients, these may be released gradually, e.g. to improve
CC compatibility. The present sequence represents a peptide ligand, which is
CC circularised by a disulphide bond
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 34
ABG70754
ID ABG70754 standard; peptide; 9 AA.
XX
AC ABG70754;
XX
DT 28-NOV-2002 (first entry)
XX
DE Targeting moiety peptide motif #1.
XX
KW Diagnostic; negatively charged carrier; targeting moiety; tumour;
KW endothelial tumour; microbiological organism; cyclic.
XX
OS Synthetic.
XX
PN EP1209469-A1.
XX
PD 29-MAY-2002.
XX
PF 22-NOV-2001; 2001EP-00127384.
XX
PR 22-NOV-2000; 2000US-0252666P.
XX
PA (VECT-) VECTRON THERAPEUTICS AG.
XX
PI Bruesselbach S, Fahr A, Graser A;
XX
DR WPI; 2002-683934/74.
XX
PT Diagnostic system for diagnosing e.g. tumors has a carrier, targeting
PT moiety and diagnostic agent.
XX
PS Example 8; Page 10; 30pp; English.
XX
CC The invention discloses a diagnostic system comprising at least one
CC negatively charged carrier, a targeting moiety and a diagnostic agent.
CC The diagnostic kit comprises at least one negatively charged carrier and

CC diagnostic agent. The system is useful for diagnosis of disease e.g.
CC tumours, particularly endothelial tumours and for in vivo diagnosis (in
CC cells and tissues) and diagnosis of microbiological organisms in vitro.
CC The system improves the persistence of the diagnostic agent in the cell
CC or tissue, has a long shelf life and a low toxicity. The sequence
CC presented is the targeting moiety peptide motif #1
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 35
AAU75609
ID AAU75609 standard; peptide; 9 AA.
XX
AC AAU75609;
XX
DT 08-MAY-2002 (first entry)
XX
DE Synthetic peptide used in binding assay of Tumstatin-45-132.
XX
KW Human; type IV collagen alpha 3 chain; cytostatic; antiangiogenic;
KW non-Goodpasture fragment; alpha3(IV)NC1 domain; alphavbeta3 integrin;
KW endothelial cell proliferation; apoptosis; Arresten; Canstatin;
KW Tumstatin; angiogenesis; tumour.
XX
OS Synthetic.
XX
PN WO200151523-A2.
XX
PD 19-JUL-2001.
XX
PF 08-JAN-2001; 2001WO-US000565.
XX
PR 07-JAN-2000; 2000US-00479118.
PR 04-APR-2000; 2000US-00543371.
PR 21-JUL-2000; 2000US-00625191.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Kalluri R;
XX
DR WPI; 2002-188037/24.
XX
PT A non-Goodpasture fragment of alpha3(IV)NC1 domain used in detecting and
PT treating disorders involving angiogenesis.
XX
PS Example 45; Page 143; 205pp; English.
XX
CC The invention relates to a non-Goodpasture fragment of alpha3(IV)NC1
CC domain, having one or more of the characteristics selected from: (a) the
CC ability to bind alphavbeta3 integrin; (b) the ability to inhibit
CC proliferation of endothelial cells; and (c) the ability to cause
CC apoptosis of endothelial cells. Also described are the following: (1) use
CC of Arresten, Canstatin or Tumstatin, or a fragment, mutant, homologue,
CC analogue or allelic variant in the preparation of a medicament for
CC treating a disorder involving: (a) inhibiting angiogenesis in a tissue,
CC where the angiogenesis is mediated by one or more endothelial cell
CC integrins or one or more endothelial cell integrin subunits; or (b) by
CC promoting or inducing endothelial cell apoptosis in a tissue, where the
CC endothelial cell apoptosis is mediated by one or more endothelial cell
CC integrins or one or more endothelial cell integrin subunits; (2) use of
CC an antibody or peptide that specifically binds the alpha1, alpha2,
CC alpha3, alpha5, alpha6, alphav, beta1 or beta3 subunit of integrin in the
CC preparation of a medicament for inhibiting angiogenesis or cell
CC proliferation; (3) use of an inhibitor, such as an antibody, antibody
CC fragment or peptide of receptor-mediated angiogenesis in the preparation
CC of a medicament for treating a proliferative disease in a vertebrate,
CC where the disease is characterised by angiogenesis that is mediated by
CC receptors to Arresten, Canstatin or Tumstatin and where the receptors
CC inhibited are Arresten, Canstatin or Tumstatin receptors; (4) use of one
CC or more soluble receptors that bind Arresten, Canstatin or Tumstatin in
CC the presence of a medicament for promoting angiogenesis in a tissue; and
CC (5) use of integrins in the preparation of a medicament for promoting or
CC inducing angiogenesis or cell proliferation in a tissue. The fragments
CC Arresten, Canstatin or Tumstatin and their mutants, homologues, analogues
CC or allelic variants are useful in the preparation of a medicament for
CC treating a disorder involving inhibiting angiogenesis in a tissue, where
CC the angiogenesis is mediated by one or more endothelial cell integrins or
CC one or more endothelial cell integrin subunits; or by promoting or
CC inducing endothelial cell apoptosis in a tissue, where the endothelial
CC cell apoptosis is mediated by one or more endothelial cell integrins or
CC one or more endothelial cell integrin subunits. The medicament is useful
CC in inhibiting tumour growth and for the regression of an established
CC tumour. The present sequence represents a synthetic peptide used in a
CC binding assay of human type IV collagen alpha 3 chain mutant, Tumstatin-
CC 45-132
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 36
AAU79138
ID AAU79138 standard; peptide; 9 AA.
XX
AC AAU79138;
XX
DT 18-JUN-2002 (first entry)
XX
DE Synthetic peptide #38 used for production of cancer treating kit.
XX
KW Cyclic; cytostatic; tumour neovasculature; receptor; binder; cancer;
KW anticancer agent; radiosensitiser agent; photodynamic therapy;
KW tumour imaging; angiogenesis; rheumatoid arthritis; kit; alpha-v-beta3;
KW alpha-v-beta5.
XX
OS Synthetic.
XX
PN WO200197860-A2.
XX
PD 27-DEC-2001.
XX
PF 21-JUN-2001; 2001WO-US020108.
XX
PR 21-JUN-2000; 2000US-0213206P.
XX
PA (DUPO) DUPONT PHARM CO.
XX
PI Rajopadhye M, Edwards DS, Barrett JA, Carpenter AP, Heminway SJ;
PI Liu S, Singh P;
XX
DR WPI; 2002-195659/25.
XX
PT Kit used for treating cancer comprises peptide compound and anticancer
PT and/or radiosensitizer agent.
XX
PS Disclosure; Page 106; 306pp; English.
XX
CC The present invention relates to a new kit which comprises a peptide
CC compound, an anticancer agent and/or radiosensitiser agent and a carrier.
CC The kit of the invention can be used for treating cancer, preferably in

```
CC   combination with photodynamic therapy, for tumour imaging and for
CC   monitoring the progress and results of therapeutic angiogenesis
CC   treatment. The invention is also used for treating rheumatoid arthritis.
CC   The present amino acid sequence represents one of a collection of
CC   peptides (AAU79101-AAU79139) used in the methods of the invention for the
CC   production of kits used for treating cancer. The present sequence binds
CC   alpha-v-beta3 and alpha-v-beta5
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 37
AAU98972
ID   AAU98972 standard; peptide; 9 AA.
XX
AC   AAU98972;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Adeno-associated virus (AAV) targeting peptide #1.
XX
KW   Adeno-associated virus 2 vector; AAV2; cancer; VP1 capsid;
KW   heparin-sulphate proteoglycan; vaccine; immune response; ovarian cancer;
KW   cyclic.
XX
OS   Synthetic.
XX
PN   WO200253703-A2.
XX
PD   11-JUL-2002.
XX
PF   04-JAN-2002; 2002WO-US000152.
XX
PR   05-JAN-2001; 2001US-0260124P.
XX
PA   (CHIL-) CHILDRENS HOSPITAL INC.
XX
PI   Bartlett JS;
XX
DR   WPI; 2002-583608/62.
XX
PT   New adeno-associated virus vector comprises a biotinylated capsid or
PT   capsid protein with an amino acid insertion in the VP1 capsid, useful as
PT   a vaccine or for transferring a therapeutic peptide to a cancer cell.
XX
PS   Claim 10; Page 38; 57pp; English.
XX
CC   The invention relates to an adeno-associated virus (AAV) vector (I)
CC   comprising a biotinylated capsid or capsid protein (II) with an amino
CC   acid insertion following the capsid amino acid at position 139, 161, 588
CC   or 657 in the VP1 capsid. The AAV vector comprises a capsid protein
CC   containing one or more amino acid insertions that ablate the ability of
CC   the vector to bind heparin-sulphate proteoglycan and allow the vector to
CC   use a cellular receptor not used by wild type AAV. Modified (I) are
CC   useful as vaccines to elicit immune responses to amino acids, where the
CC   response can be protective and/or therapeutic. (I) may be used to
CC   transfer a therapeutic peptide to a cancer cell, particularly to an
CC   ovarian cancer cell. The present sequence represents an AAV targeting
CC   peptide used to make mutant AAV vectors of the invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 38
AAM48795
ID   AAM48795 standard; peptide; 9 AA.
XX
AC   AAM48795;
XX
DT   08-APR-2002  (first entry)
XX
DE   Tumour-targetting peptide vector peptide SEQ ID NO 1.
XX
KW   Tumour; integrin; histidinated polylysine; cytostatic; peptide targeting;
KW   cancer.
XX
OS   Synthetic.
XX
PN   JP2001309790-A.
XX
PD   06-NOV-2001.
XX
PF   02-MAY-2000; 2000JP-00134059.
XX
PR   02-MAY-2000; 2000JP-00134059.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-134852/18.
XX
PT   Tumor-targeting peptide vector for diagnosing and treating progressive
PT   solid cancer, comprises a peptide having a ligand motif of integrin and a
PT   peptide having histidinated polylysine.
XX
PS   Disclosure; Page 4; 8pp; Japanese.
XX
CC   The invention relates to a tumour-targeting peptide vector comprising a
CC   peptide containing a ligand motif of integrin combined with a peptide
CC   consisting of histidinated polylysine and where the histidinated
CC   polylysine has 20 to 40 lysine residues and one histidine is added to 4
CC   lysine residues. The peptide vector has cytostatic activity and can be
CC   used for the treatment of progressive solid cancer patients and the
CC   diagnosis of progressive solid cancers. The present sequence is that of a
CC   peptide of the invention
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 39
ABB79525
ID   ABB79525 standard; peptide; 9 AA.
XX
AC   ABB79525;
XX
DT   23-SEP-2002  (first entry)
XX
DE   RGD motif-containing peptide.
XX
KW   RGD motif; integrin; tumour; metastasis; imaging.
XX
OS   Unidentified.
XX
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PN WO200247537-A2.
XX
PD 20-JUN-2002.
XX
PF 11-DEC-2001; 2001WO-US048157.
XX
PR 11-DEC-2000; 2000US-00734628.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Chinnaiyan AM, Rehemtulla A, Ross BD;
XX
DR WPI; 2002-547820/58.
XX
PT Chimeric molecule useful in situ and in vivo imaging of cells and tissues
PT e.g. tumor tissues comprises a first domain and a second domain.
XX
PS Claim 9; Page 25; 35pp; English.
XX
CC The present sequence is that of a peptide including the tripeptide Arg-
CC Gly-Asp (RGD) motif that is often the primary site of recognition by
CC integrins that are expressed on tumour cells and which are responsible
CC for tumour invasion and metastasis. Imaging of cells that can
CC specifically bind to RGD-expressing peptide and polypeptide ligands in
CC vivo can identify tumour cells and tumour blood vessels. A claimed
CC chimeric molecule consists of: a first domain comprising a fluorescent,
CC bioluminescent or chemiluminescent polypeptide or a heterologous kinase;
CC and a second domain comprising an RGD motif-containing polypeptide, a
CC selectin-binding polypeptide, a matrix metalloproteinase-binding
CC polypeptide, or a chondroitin sulfate proteoglycan-binding polypeptide,
CC where the RGD motif-containing polypeptide preferably comprises the
CC present amino acid sequence. The chimeric molecule is used in methods and
CC compositions for imaging cells and tissues in vivo and in situ, and
CC especially for identifying sites of primary and metastatic tumours and
CC tumour neovasculature. The chimeric molecules enhance the imaging of
CC cells and tissues by, e.g., computer assisted tomography (CAT), magnetic
CC resonance spectroscopy (MRS), magnetic resonance imaging (MRI), positron
CC emission tomography (PET), single-photon emission computed tomography
CC (SPECT) or bioluminescence imaging
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 40
ABG31063
ID ABG31063 standard; peptide; 9 AA.
XX
AC ABG31063;
XX
DT 05-NOV-2002 (first entry)
XX
DE Alpha v beta 3 integrin binding peptide.
XX
KW Angiogenesis; peptide domain display library; ischaemia; wound; ulcer;
KW neovascularisation; arthritis; diabetes; cancer; human;
KW alpha v beta 3 integrin.
XX
OS Homo sapiens.
XX
PN WO200246213-A2.
XX
PD 13-JUN-2002.
XX
PF 07-NOV-2001; 2001WO-US051389.
XX
PR 07-NOV-2000; 2000US-0246461P.
XX
PA (GPCB-) GPC BIOTECH INC.
XX
PI Gyuris J;
XX
DR WPI; 2002-599456/64.
XX
PT Isolating peptide domains (PD)s, useful for modulating angiogenesis, by
PT utilizing PD display library which may be used in both display mode
PT attached to microorganism surface, and in secretion mode such that PDs
PT are secreted in soluble form.
XX
PS Disclosure; Page 72; 98pp; English.
XX
CC The invention describes a method of isolating a peptide domain that
CC modulates angiogenic activity comprising utilising a peptide domain
CC display library. The method is most preferably useful for isolating a
CC peptide domain capable of inhibiting angiogenic activity. The invention
CC also describes a method useful for modulating angiogenic process in an
CC animal. This method is useful for treating a patient suffering from
CC ischaemia, wound and ulcers which require increased angiogenesis or
CC neovascularisation and for treating patients suffering from arthritis,
CC diabetes and cancer in which prevention of new blood vessel formation or
CC reduction in the number of existing blood vessels, is desired. The
CC display mode and secretion mode can be carried out without the need to
CC sub-clone the test peptide domain coding sequence into another vector.
CC The method also reduces the loss of peptide domain sequences from the sub
CC -library by eliminating sub-cloning steps. This sequence represents an
CC alpha v beta 3 integrin binding peptide containing the RGD motif
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 41
AAG78427
ID AAG78427 standard; peptide; 9 AA.
XX
AC AAG78427;
XX
DT 25-APR-2002 (first entry)
XX
DE Cyclic peptide that binds to alpha-V-beta-3 and alpha-V-beta-5.
XX
KW Basic FGF receptor; bFGFR; macrocyclic chelant; growth factor;
KW metallopharmaceutical; cardiovascular disorder; infection; disease;
KW heavy metal detoxification; medical imaging modality; cytostatic; cyclic;
KW cancer.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "linked to residue 6 to form cyclic peptide"
FT Misc-difference 6
FT /note= "linked to residue 1 to form cyclic peptide"
XX
PN WO200177102-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011388.
XX
PR 07-APR-2000; 2000US-0195234P.
XX

PA (DUPO) DUPONT PHARM CO.
XX
PI Liu S;
XX
DR WPI; 2002-049126/06.
XX
PT New macrocyclic chelants, useful for treating cancer, diagnosing
PT thromboembolic disorders, atherosclerosis, infection, inflammation and
PT transplant rejection, detecting new angiogenic vasculature and metal
PT detoxification.
XX
PS Disclosure; Page 84; 136pp; English.
XX
CC This invention relates to macrocyclic chelants and their salts. They are
CC useful in compositions for treating cancer, diagnosing thromboembolic
CC disorders, atherosclerosis, infections, inflammation and transplant
CC rejection, and for detecting new angiogenic vasculature and metal
CC detoxification. This peptide sequence represents a cyclic peptide that
CC binds to alpha-V-beta-3 and alpha-V-beta-5
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 42
AAM51995
ID AAM51995 standard; peptide; 9 AA.
XX
AC AAM51995;
XX
DT 12-FEB-2002 (first entry)
XX
DE Drug targeting peptide RGD-4C.
XX
KW Targeting vector; angiogenesis associated receptor; integrin receptor;
KW alphavbeta3; cancer; heart disease; atherosclerosis; inflammation;
KW rheumatoid arthritis; gingivitis; osteoarthritis; psoriasis; cytostatic;
KW antiinflammatory; antiarteriosclerotic; antirheumatic; antiarthritic;
KW anti-HIV; osteopathic; antipsoriatic; antidiabetic; opthalmological;
KW dermatological; antiulcer; ulcerative colitis.
XX
OS Synthetic.
XX
PN WO200177145-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-NO000146.
XX
PR 12-APR-2000; 2000GB-00009042.
PR 12-OCT-2000; 2000GB-00025070.
XX
PA (NYCO-) NYCOMED IMAGING AS.
XX
PI Cuthbertson A, Indrevoll B;
XX
DR WPI; 2002-049128/06.
XX
PT New peptide-based compounds useful as a diagnostic imaging agent
PT comprises affinity for integrin receptors.
XX
PS Disclosure; Page 5; 63pp; English.
XX
CC The present invention relates to peptide-based compounds which have
CC affinity for integrin receptors, particularly the integrin alphavbeta3
CC receptor. These can be used in the manufacture of a contrast medium for
CC use as a diagnostic imaging agent for generating images of a human or non
CC -human animal for treating cancer or a related disease, and as targeting
CC vectors that bind to receptors associated with angiogenesis. Diseases and
CC indications associated with angiogenesis include arteriovenous
CC malformations, astrocytomas, choriocarcinomas, glioblastomas, gliomas,
CC hemangiomas (childhood capillary), hepatomas, hyperplastic endometrium,
CC ischaemic myocardium, kaposi sarcoma, macular degeneration, melanoma,
CC neuroblastomas, occluding peripheral artery disease, osteoarthritis,
CC psoriasis, retinopathy (diabetic, proliferative), scleroderma, seminomas,
CC rheumatoid arthritis, atherosclerosis, inflammation, gingivitis and
CC ulcerative colitis. The present sequence is a peptide which can be used
CC in a compound of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 43
ABG73024
ID ABG73024 standard; peptide; 9 AA.
XX
AC ABG73024;
XX
DT 28-FEB-2003 (first entry)
XX
DE Integrin Alpha5Beta3 subunit antagonist #4.
XX
KW Vitronectin receptor; cardiac perfusion; imaging agent;
KW perfusion imaging agent; tricine; TPPTS; angiogenesis; organ perfusion;
KW tris(3-sulphonatophenyl)phosphine trisodium salt; vulnerable plaque;
KW perfusion abnormality; endothelial damage; cancer; brain perfusion;
KW integrin Alpha5Beta3 subunit; antagonist.
XX
OS Synthetic.
XX
PN US2002106325-A1.
XX
PD 08-AUG-2002.
XX
PF 27-NOV-2001; 2001US-00995388.
XX
PR 27-NOV-2000; 2000PH-00007201.
XX
PA (CARP/) CARPENTER A P.
XX
PI Carpenter AP;
XX
DR WPI; 2003-057227/05.
XX
PT Simultaneous imaging using vitronectin receptor targeted and perfusion
PT imaging agent, useful for imaging sites of angiogenesis, organ perfusion,
PT endothelial damage, site of vulnerable plaque and perfusion
PT abnormalities.
XX
PS Disclosure; Page 21; 86pp; English.
XX
CC The invention relates to a method of concurrent imaging involving
CC administration of a vitronectin receptor targeted imaging agent and a
CC perfusion imaging agent, detection of both agents and formation of a
CC combined image. Also included is a kit comprising: (i) a compound (I) or
CC (II) where the compound comprises: (1) a chelator capable of chelating
CC the metal; (2) a targeting moiety where the targeting moiety is bound to
CC the chelator, and (3) 0-1 linking groups between the targeting moiety and
CC the chelator, and where the targeting moiety is a peptide or
CC peptidomimetic which binds to a vitronectin receptor; (ii) a reducing
CC agent (preferably tin (II)); (iii) one or more ancillary ligands

CC (preferably tricine or tris(3-sulphonatophenyl)phosphine trisodium salt
CC (TPPTS). The method is for use in concurrent imaging sites of
CC angiogenesis, organ perfusion, in diagnosing and localising sites of
CC angiogenesis and perfusion abnormalities, in concurrent detection and
CC localisation of sites of vulnerable plaque and perfusion abnormalities,
CC and of endothelial damage. The method is also useful for diagnosis and
CC treatment of cancer. The perfusion imaging agents include cardiac and
CC brain perfusion agents. The combination of a vitronectin targeted imaging
CC agent and the perfusion imaging agent provide additive or synergistic
CC therapeutic response without unacceptable additive toxicity. There is
CC also a much lower systemic radiation exposure to the patient. The present
CC sequence is a integrin Alpha5Beta3 subunit antagonist included in the
CC specification
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 44
ABB84641
ID ABB84641 standard; peptide; 9 AA.
XX
AC ABB84641;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human integrin peptide SEQ ID 1.
XX
KW Integrin; human; image enhancing agent; selectin; bioluminescence image;
KW matrix metalloproteinase; MMP; chondroitin sulphate proteoglycan;
KW computer assisted tomography; CAT; magnetic resonance spectroscopy; MRS;
KW magnetic resonance imaging; MRI; positron emission tomography; PET;
KW single-photon emission computed tomography; SPECT; BLI;
KW tumour neovasculature; anti-tumour; cell growth disorder; cancer.
XX
OS Homo sapiens.
XX
PN US2002122806-A1.
XX
PD 05-SEP-2002.
XX
PF 05-MAR-2001; 2001US-00734628.
XX
PR 05-MAR-2001; 2001US-00734628.
XX
PA (CHIN/) CHINNAIYAN A M.
PA (REHE/) REHEMTULLA A.
PA (ROSS/) ROSS B D.
XX
PI Chinnaiyan AM, Rehemtulla A, Ross BD;
XX
DR WPI; 2003-066773/06.
XX
PT Novel chimeric molecule for imaging sites of primary/metastatic tumors
PT and tumor neovasculature, comprises first domain having e.g. fluorescent
PT polypeptide and second domain having e.g. selectin-binding polypeptide.
XX
PS Claim 9; Page 10; 15pp; English.
XX
CC This invention describes a novel chimeric molecule comprising a first
CC domain having an image enhancing agent e.g. a fluorescent, bioluminescent
CC or chemiluminescent polypeptide, or a heterologous kinase, and a second
CC domain comprising RGD motif-comprising polypeptide, selectin-binding
CC polypeptide, matrix metalloproteinase (MMP)-binding polypeptide or
CC chondroitin sulphate proteoglycan-binding polypeptide. The molecule of
CC the invention can be used in a pharmaceutical formulation capable of
CC binding to a cell, a tissue or an organ in a cell-, tissue- or organ-
CC specific manner, which enhances a computer assisted tomography (CAT)
CC image, a magnetic resonance spectroscopy (MRS) image, a magnetic
CC resonance imaging (MRI) image, a positron emission tomography (PET)
CC image, a single-photon emission computed tomography (SPECT) image or a
CC bioluminescence image (BLI). The formulation can be used for in situ or
CC in vivo imaging of a cell, tissue (tumour tissue) or organ or a full
CC body, useful for in vivo imaging of tumour neovasculature in an
CC individual and for in vivo screening of anti-tumour agents. The product
CC of the invention is useful for non-invasively evaluating the
CC effectiveness of therapy for disorders of cell growth, such as cancer.
CC This sequence represents a human integrin-derived peptide used to
CC illustrate the method of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 45
ABU59556
ID ABU59556 standard; peptide; 9 AA.
XX
AC ABU59556;
XX
DT 22-APR-2003 (first entry)
XX
DE Tumour angiogenic epithelium-targeting peptide #1.
XX
KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
KW tumour; cationic cancer-targeting peptide.
XX
OS Synthetic.
XX
PN US2002041898-A1.
XX
PD 11-APR-2002.
XX
PF 25-JUL-2001; 2001US-00912609.
XX
PR 05-JAN-2000; 2000US-00478124.
PR 31-OCT-2000; 2000US-00703474.
XX
PA (UNGE/) UNGER E C.
PA (MATS/) MATSUNAGA T O.
PA (RAMA/) RAMASWAMI V.
PA (ROMA/) ROMANOWSKI M J.
XX
PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX
DR WPI; 2003-208921/20.
XX
PT Targeted delivery system comprising a bioactive agent homogeneously
PT dispersed in a targeted matrix is especially useful in cancer therapy.
XX
PS Claim 46; Page 38; 46pp; English.
XX
CC The invention relates to a composition comprising a bioactive agent
CC homogeneously dispersed in a targeted matrix (polymer and targeting
CC ligand). Also included are a targeted matrix for use as a delivery
CC vehicle comprising a polymer associated with a targeting ligand,
CC enhancing the bioavailability of an agent comprising administration of
CC the composition and treating cancer comprising administration of the
CC novel composition. The method is useful for targeted delivery of a drug,
CC especially in cancer therapy. The targeting ligand may be a peptide.

CC Examples of targeting peptides are disclosed including cathepsin-D
CC substrate peptides, peptides targeting receptors in the brain and kidney,
CC peptides recognising fibronectin- and vitronectin-binding integrins,
CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
CC peptides targeting the angiogenic endothelium of solid tumours, tissue
CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
CC adrenal gland and retina), and cationic cancer- targeting peptides. The
CC present sequence is a peptide targeting ligand disclosed in the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 46
ABU08571
ID ABU08571 standard; peptide; 9 AA.
XX
AC ABU08571;
XX
DT 05-JUN-2003 (first entry)
XX
DE RGD-containing, tumour targeting peptide #1.
XX
KW TNF related apoptosis inducing ligand; TRAIL; integrin;
KW tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;
KW antiinflammatory; dermatological; thrombotic microangiopathy;
KW thrombotic thrombocytopaenic purpura; TTP; HUS; SLE; clotting disorder;
KW adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
KW systemic lupus erythematosus; tumour targeting peptide.
XX
OS Unidentified.
XX
PN US6521228-B1.
XX
PD 18-FEB-2003.
XX
PF 02-APR-2001; 2001US-00825563.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
PR 25-JUN-1996; 96US-00670354.
PR 26-MAR-1998; 98US-00048641.
PR 10-NOV-1998; 98US-00190046.
PR 26-MAY-1999; 99US-00320424.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Wiley SR, Goodwin RG;
XX
DR WPI; 2003-340628/32.
XX
PT Novel antibody which binds to human tumor necrosis factor related
PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated
PT apoptosis of a target cell, or blocking binding of TRAIL to a target
PT cell.
XX
PS Disclosure; Col 11; 40pp; English.
XX
CC The invention relates to an antibody that specifically binds: (a) the
CC human tumor necrosis factor (TNF) related apoptosis inducing ligand
CC (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL
CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of
CC ABU08558, or (d) a fragment of the TRAIL protein. Also included is an
CC antigen-binding fragment of the antibody (a monoclonal antibody), a
CC hybridoma cell line that produces the antibody. The antibody is used in
CC assays to detect the presence of TRAIL polypeptides, either in vitro or
CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of
CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
CC The antibody is useful for treating disorders mediated or exacerbated by
CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic
CC thrombocytopaenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
CC (even though it can strike children as well) small blood vessel clotting
CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic
CC lupus erythematosus (SLE). The present sequence is an RGD (Arg-Gly-Asp)
CC containing, tumour targeting, peptide which is used in fusion proteins
CC with TRAIL to allow the fusion protein to bind to alpha integrins
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
||||||||| |
Db 1 CDCRGDCFC 9

RESULT 47
ABP60343
ID ABP60343 standard; peptide; 9 AA.
XX
AC ABP60343;
XX
DT 20-FEB-2003 (first entry)
XX
DE Tumour vasculature integrin alpha-v-beta-3 or 5 targeting peptide 8.
XX
KW Radiopharmaceutical; ascorbic acid; tumour; vasculature;
KW integrin alpha-v-beta-3.
XX
OS Synthetic.
XX
PN US2002122769-A1.
XX
PD 05-SEP-2002.
XX
PF 22-FEB-2002; 2002US-00081258.
XX
PR 26-FEB-2001; 2001US-0271389P.
XX
PA (LIUS/) LIU S.
XX
PI Liu S;
XX
DR WPI; 2003-119656/11.
XX
PT Buffering, chelating and stabilizing radiopharmaceutical involves
PT contacting radiopharmaceutical with ascorbic acid analogs.
XX
PS Disclosure; Page 10; 21pp; English.
XX
CC The invention relates to buffering, chelating and stabilising a
CC radiopharmaceutical by contacting the radiopharmaceutical with ascorbic
CC acid analogues. The invention also includes a radiopharmaceutical
CC composition comprising a radiolabelled chelator-biomolecule conjugate of
CC formula M-Ch-Ln-(BM)_m, where: M = metallic isotope; Ch = metal chelator;
CC Ln = optional linking group; BM = biomolecule; and m = 1-10. The present
CC sequence is that of a tumour vasculature integrin alpha-v-beta-3 or 5
CC targeting peptide, which can be included as the BM part of the
CC radiopharmaceutical composition of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9

```
                  |||||||||
Db          1 CDCRGDCFC 9


RESULT 48
ADA20234
ID   ADA20234 standard; peptide; 9 AA.
XX
AC   ADA20234;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Synthetic peptide Seq ID35 related to human type IV collagen alpha.
XX
KW   anti-angiogenic; undesirable angiogenesis; capillary; tumour growth;
KW   metastasis; basement membrane organisation; type IV collagen network;
KW   C-terminal globular non-collagenous domain; NC1; type IV collagen;
KW   cell surface receptor; integrin; angiogenic activity; protein synthesis;
KW   cytostatic; gene therapy.
XX
OS   Synthetic.
XX
PN   WO2003059257-A2.
XX
PD   24-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-US040938.
XX
PR   21-DEC-2001; 2001US-00032221.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Kalluri R;
XX
DR   WPI; 2003-587256/55.
XX
PT   New peptide, useful for preparing a composition for inhibiting tumor
PT   growth, angiogenic activity or protein synthesis in a mammalian tissue.
XX
PS   Example 45; Page 142; 240pp; English.
XX
CC   This invention relates to novel isolated proteins and their fragments
CC   with anti-angiogenic properties. The invention also relates to the DNA
CC   sequences which encode the novel proteins. A wide variety of diseases are
CC   the result of undesirable angiogenesis. The formation of new capillaries
CC   from pre-existing vessels is essential for tumour growth and metastasis.
CC   Basement membrane organisation is dependent on the assembly of a type IV
CC   collagen network which may occur through the C-terminal globular non-
CC   collagenous (NC1) domain of type IV collagen. The alpha 1 and alpha 2
CC   forms are ubiquitously exhibited in human basement membranes. In the
CC   present invention, cell surface receptors (in particular integrins) which
CC   specifically bind anti-angiogenic proteins and peptides (in particular
CC   the alpha 1, alpha 2 and alpha 3 domains of the NC1 domain of type IV
CC   collagen) are disclosed. The proteins of the invention may inhibit tumour
CC   growth, angiogenic activity in mammalian tissue or protein synthesis in
CC   endothelial cells and thus may exhibit cytostatic activity. The DNA
CC   sequences of the invention may be useful in gene therapy. The present
CC   sequence is that of a synthetic peptide (Seq ID35) which was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 49
ADC44955
ID   ADC44955 standard; peptide; 9 AA.
XX
AC   ADC44955;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Endothelial cell binding associated control peptide SEQ ID NO:685.
XX
KW   endothelial cell binding protein; ECBP; anti-tumour; cytostatic;
KW   vasotropic; antipsoriatic; dermatological; ophthalmological;
KW   antidiabetic; antiarthritic; vulnerary; antiulcer; antiinflammatory;
KW   antibacterial; gynaecological; angiogenesis.
XX
OS   Synthetic.
XX
PN   WO2003037172-A2.
XX
PD   08-MAY-2003.
XX
PF   01-NOV-2002; 2002WO-US035258.
XX
PR   01-NOV-2001; 2001US-0334822P.
XX
PA   (GPCB-) GPC BIOTECH INC.
XX
PI   Gyuris J,  Lamphere L,  Morris AJ,  Tsaioun K;
XX
DR   WPI; 2003-482072/45.
XX
PT   Novel synthetic or recombinant polypeptide useful for promoting, reducing
PT   proliferation and/or migration of endothelial cells, and for modulating
PT   angiogenesis, has endothelial cell binding protein sequences.
XX
PS   Disclosure; SEQ ID NO 685; 126pp; English.
XX
CC   The invention relates to a novel isolated, synthetic or recombinant
CC   peptide or polypeptide which includes one or more endothelial cell
CC   binding protein (ECBP) sequences. A peptide of the invention has anti-
CC   tumour, cytostatic, vasotropic, antipsoriatic, dermatological,
CC   ophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer,
CC   antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC   is useful for promoting, reducing the proliferation and/or migration of
CC   endothelial cells, by treating the cells with an ECBP agonist, which is
CC   preferably the peptide, to promote proliferation and/or migration of the
CC   treated cells, and for reducing or promoting angiogenesis, by treating
CC   the cells with an ECBP antagonist, which is preferably the peptide of the
CC   invention. A peptide of the invention is also useful for manufacturing a
CC   medicament for promoting angiogenesis, by admixing an ECBP agonist or
CC   ECBP antagonist to promote or reduce angiogenesis at one or more sites in
CC   a treated mammal. The medicament is useful for promoting or reducing
CC   angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
CC   of a viral particle. The present sequence represents an ECBP of the
CC   invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 65;  DB 7;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


Search completed: July 11, 2004, 10:08:50
Job time : 52 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 10:01:23 ; Search time 45 Seconds
(without alignments)
62.384 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 116305

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	9	9	US-09-765-086-1	Sequence 1, Appli
2	65	100.0	9	9	US-09-845-160-5	Sequence 5, Appli
3	65	100.0	9	9	US-09-245-603A-16	Sequence 16, Appl
4	65	100.0	9	9	US-09-364-597A-16	Sequence 16, Appl
5	65	100.0	9	9	US-09-734-628-1	Sequence 1, Appli
6	65	100.0	9	9	US-09-971-798-5	Sequence 5, Appli
7	65	100.0	9	9	US-09-969-192-3	Sequence 3, Appli
8	65	100.0	9	9	US-09-840-277-38	Sequence 38, Appl
9	65	100.0	9	9	US-09-840-277-62	Sequence 62, Appl
10	65	100.0	9	10	US-09-801-485-2	Sequence 2, Appli
11	65	100.0	9	10	US-09-791-524-124	Sequence 124, App
12	65	100.0	9	12	US-10-609-217-450	Sequence 450, App
13	65	100.0	9	12	US-10-609-217-1076	Sequence 1076, Ap
14	65	100.0	9	12	US-10-363-208-166	Sequence 166, App
15	65	100.0	9	12	US-10-632-388-450	Sequence 450, App
16	65	100.0	9	12	US-10-632-388-1076	Sequence 1076, Ap
17	65	100.0	9	12	US-10-652-244-20	Sequence 20, Appl
18	65	100.0	9	12	US-10-651-723-450	Sequence 450, App
19	65	100.0	9	12	US-10-651-723-1076	Sequence 1076, Ap
20	65	100.0	9	12	US-09-912-609-31	Sequence 31, Appl
21	65	100.0	9	12	US-09-995-388-47	Sequence 47, Appl
22	65	100.0	9	12	US-10-013-009-1	Sequence 1, Appli
23	65	100.0	9	12	US-10-033-769-10	Sequence 10, Appl
24	65	100.0	9	12	US-10-269-575-1	Sequence 1, Appli
25	65	100.0	9	12	US-10-645-761-450	Sequence 450, App
26	65	100.0	9	12	US-10-645-761-1076	Sequence 1076, Ap
27	65	100.0	9	13	US-10-080-854-8	Sequence 8, Appli
28	65	100.0	9	13	US-10-038-972A-10	Sequence 10, Appl
29	65	100.0	9	14	US-10-304-160-3	Sequence 3, Appli
30	65	100.0	9	14	US-10-264-374-1	Sequence 1, Appli
31	65	100.0	9	14	US-10-032-221B-35	Sequence 35, Appl
32	65	100.0	9	14	US-10-375-992-1	Sequence 1, Appli
33	65	100.0	9	16	US-10-666-696-450	Sequence 450, App
34	65	100.0	9	16	US-10-666-696-1076	Sequence 1076, Ap
35	65	100.0	9	16	US-10-653-048-450	Sequence 450, App
36	65	100.0	9	16	US-10-653-048-1076	Sequence 1076, Ap
37	65	100.0	9	16	US-10-264-374-1	Sequence 1, Appli
38	59	90.8	9	9	US-09-364-597A-17	Sequence 17, Appl
39	59	90.8	9	9	US-09-840-277-63	Sequence 63, Appl
40	59	90.8	9	12	US-10-609-217-451	Sequence 451, App
41	59	90.8	9	12	US-10-632-388-451	Sequence 451, App
42	59	90.8	9	12	US-10-651-723-451	Sequence 451, App
43	59	90.8	9	12	US-10-645-761-451	Sequence 451, App
44	59	90.8	9	16	US-10-666-696-451	Sequence 451, App
45	59	90.8	9	16	US-10-653-048-451	Sequence 451, App

ALIGNMENTS

RESULT 1
US-09-765-086-1
; Sequence 1, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 2
US-09-845-160-5

; Sequence 5, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
; APPLICANT: MIZUGUCHI, HIROYUKI
; APPLICANT: HAYAKAWA, TAKAO
; TITLE OF INVENTION: ADENOVIRUS VECTOR
; FILE REFERENCE: 081356/0163
; CURRENT APPLICATION NUMBER: US/09/845,160
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: JP 2001-131688
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP 2000-161577
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide.
US-09-845-160-5

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 3
US-09-245-603A-16
; Sequence 16, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Krasnykh, Victor N.
; APPLICANT: Dmitriev, Igor
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
; TITLE OF INVENTION: Epitope in the HI Loop of the Fiber Knob
; FILE REFERENCE: D6080
; CURRENT APPLICATION NUMBER: US/09/245,603A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/099,801
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
; OTHER INFORMATION: into the region of the fiber gene within the HI loop.
US-09-245-603A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 4
US-09-364-597A-16
; Sequence 16, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. US20020103130A1el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 5
US-09-734-628-1
; Sequence 1, Application US/09734628
; Patent No. US20020122806A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rehemtulla, Alnawaz
; APPLICANT: Ross, Brian D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IN SITU AND
; TITLE OF INVENTION: IN VIVO IMAGING OF CELLS AND TISSUES
; FILE REFERENCE: 11203-005001
; CURRENT APPLICATION NUMBER: US/09/734,628
; CURRENT FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-734-628-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 6
US-09-971-798-5
; Sequence 5, Application US/09971798
; Patent No. US20020132769A1
; GENERAL INFORMATION:
;  APPLICANT: No. US20020132769A1artis AG
;  TITLE OF INVENTION: Targeting molecules
;  FILE REFERENCE: 4-31615/GTI
;  CURRENT APPLICATION NUMBER: US/09/971,798
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-971-798-5

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 7
US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. US20020151027A1
;   GENERAL INFORMATION:
;        APPLICANT: WICKHAM, THOMAS J.
;                   ROELVINK, PETRUS W.
;                   KOVESDI, IMRE
;        TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                            CONSTRAINED PEPTIDE MOTIFS
;        NUMBER OF SEQUENCES: 80
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;             STREET: Two Prudential Plaza - 49th Floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/969,192
;             FILING DATE: 01-Oct-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 9-455061
;             FILING DATE: 06-DEC-1999
;             APPLICATION NUMBER: US 9-130225
;             FILING DATE: 06-AUG-1998
;             APPLICATION NUMBER: US 8-701124
;             FILING DATE: 21-AUG-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hefner, M. Daniel
;             REGISTRATION NUMBER: 41,826
;             REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 8
US-09-840-277-38
; Sequence 38, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-38

  Query Match             100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 9
US-09-840-277-62
; Sequence 62, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  KOHNO, TADAHIKO
;  APPLICANT:  LACEY, DAVID LEE
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
;  FILE REFERENCE: A-688A
;  CURRENT APPLICATION NUMBER: US/09/840,277
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/198,919
;  PRIOR FILING DATE: 2000-04-21
;  PRIOR APPLICATION NUMBER: 60/201,394
;  PRIOR FILING DATE: 2000-05-03
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 9
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-62

  Query Match           100.0%;  Score 65;  DB 9;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 10
US-09-801-485-2
; Sequence 2, Application US/09801485
; Publication No. US20030077818A1
; GENERAL INFORMATION:
;  APPLICANT:  Dickerson, Erin B
;  APPLICANT:  Helfand, Stuart C.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TARGETING INTERLEUKIN-12
;  TITLE OF INVENTION:  TO MALIGNANT ENDOTHELIUM
;  FILE REFERENCE:  WARF-0003
;  CURRENT APPLICATION NUMBER: US/09/801,485
;  CURRENT FILING DATE:  2001-03-08
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-801-485-2

  Query Match           100.0%;  Score 65;  DB 10;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 11
US-09-791-524-124
; Sequence 124, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
;  APPLICANT:  Aventis Pharmaceuticals Products Inc.
;  TITLE OF INVENTION:  Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
;  FILE REFERENCE:  A3319A
;  CURRENT APPLICATION NUMBER: US/09/791,524
;  CURRENT FILING DATE:  2001-02-22
;  PRIOR APPLICATION NUMBER:  60/09828
;  PRIOR FILING DATE:  1998-08-27
;  NUMBER OF SEQ ID NOS:  150
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 124
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Adenovirus
US-09-791-524-124

  Query Match           100.0%;  Score 65;  DB 10;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 12
US-10-609-217-450
; Sequence 450, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-450

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 13
US-10-609-217-1076
; Sequence 1076, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/609,217
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1076

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9
```

```
RESULT 14
US-10-363-208-166
; Sequence 166, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
;  FILE REFERENCE: 005774.P005PCT
;  CURRENT APPLICATION NUMBER: US/10/363,208
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: synthetic construct
US-10-363-208-166

  Query Match            100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 15
US-10-632-388-450
; Sequence 450, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-450

  Query Match            100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 16
US-10-632-388-1076
; Sequence 1076, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-1076

  Query Match            100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 17
US-10-652-244-20
; Sequence 20, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
;  APPLICANT: Wiley, Steven R.
;  APPLICANT:  Goodwin, Raymond G.
;  TITLE OF INVENTION: Cytokine that Induces Apoptosis
;  FILE REFERENCE: 2835-E
;  CURRENT APPLICATION NUMBER: US/10/652,244
;  CURRENT FILING DATE:  2003-09-02
;  PRIOR APPLICATION NUMBER: US/09/796,581
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/320,424
;  PRIOR FILING DATE: 1999-05-26
;  PRIOR APPLICATION NUMBER: 09/190,046
;  PRIOR FILING DATE: 1998-11-10
;  PRIOR APPLICATION NUMBER: 09/048,641
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 08/670,354
;  PRIOR FILING DATE: 1996-06-25
;  PRIOR APPLICATION NUMBER: 08/548,368
;  PRIOR FILING DATE: 1995-11-01
;  PRIOR APPLICATION NUMBER: 08/496,632
;  PRIOR FILING DATE: 1995-06-29
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: artificial
;   OTHER INFORMATION: peptide
US-10-652-244-20

  Query Match            100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
```

```
Db          1 CDCRGDCFC 9


RESULT 18
US-10-651-723-450
; Sequence 450, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-450

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 19
US-10-651-723-1076
; Sequence 1076, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-1076

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 20
US-09-912-609-31
; Sequence 31, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
;  APPLICANT: UNGER, EVAN C.
;  APPLICANT:  MATSUNAGA, TERRY ONICHI
;  APPLICANT:  RAMASWAMI, VARADARAJAN
;  APPLICANT:  ROMANOWSKI, MAREK J.
;  TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
;  FILE REFERENCE: 5030-0001.24
;  CURRENT APPLICATION NUMBER: US/09/912,609
;  CURRENT FILING DATE:  2001-07-25
;  PRIOR APPLICATION NUMBER: 09/703,474
;  PRIOR FILING DATE: 2000-10-31
;  PRIOR APPLICATION NUMBER: 09/478,124
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-912-609-31

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 21
US-09-995-388-47
; Sequence 47, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
;  APPLICANT: Carpenter, Jr., Alan P.
;  TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
;  TITLE OF INVENTION:  RECEPTOR TARGETED IMAGING AGENT
;  FILE REFERENCE: BMS-2201
;  CURRENT APPLICATION NUMBER: US/09/995,388
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: US 60/253,324
;  PRIOR FILING DATE: 2000-11-27
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-995-388-47

  Query Match           100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 22
US-10-013-009-1
```

```
; Sequence 1, Application US/10013009
; Publication No. US20020086815A1
; GENERAL INFORMATION:
;  APPLICANT: McMorris, Trevor C.
;  APPLICANT:  Kelner, Michael J.
;  TITLE OF INVENTION: Antitumor agents
;  FILE REFERENCE: 103.008US3
;  CURRENT APPLICATION NUMBER: US/10/013,009
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: US 09/386,555
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: US 09/026,633
;  PRIOR FILING DATE: 1998-02-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic amino acid sequence
US-10-013-009-1

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 23
US-10-033-769-10
; Sequence 10, Application US/10033769
; Publication No. US20020094316A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Shuang
;  TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
;  FILE REFERENCE: BMS-2204
;  CURRENT APPLICATION NUMBER: US/10/033,769
;  CURRENT FILING DATE:  2001-12-27
;  PRIOR APPLICATION NUMBER: US 60/260,619
;  PRIOR FILING DATE: 2001-01-09
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-033-769-10

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 24
US-10-269-575-1
; Sequence 1, Application US/10269575
; Publication No. US20030204049A1
; GENERAL INFORMATION:
;  APPLICANT: CUTHBERTSON, ALAN
;  APPLICANT:  INDREVOLL, BARD
;  TITLE OF INVENTION: PEPTIDE-BASED COMPOUNDS
;  FILE REFERENCE: NIDN-10433
;  CURRENT APPLICATION NUMBER: US/10/269,575
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/NO01/00146
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: GB 0009042.3
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: GB 0025070.4
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: illustrative
;   OTHER INFORMATION: peptide
US-10-269-575-1

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 25
US-10-645-761-450
; Sequence 450, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-450

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 26
US-10-645-761-1076
; Sequence 1076, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
```

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;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-1076

  Query Match             100.0%;  Score 65;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 27
US-10-080-854-8
; Sequence 8, Application US/10080854
; Publication No. US20020172940A1
; GENERAL INFORMATION:
;  APPLICANT: GYURIS, JENO
;  APPLICANT:  MORRIS, AARON J.
;  TITLE OF INVENTION: METHODS AND REAGENTS FOR ISOLATING BIOLOGICALLY ACTIVE
;  TITLE OF INVENTION:  PEPTIDES
;  FILE REFERENCE: MIV-106.01
;  CURRENT APPLICATION NUMBER: US/10/080,854
;  CURRENT FILING DATE:  2002-02-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: RGD motif
US-10-080-854-8

  Query Match             100.0%;  Score 65;  DB 13;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 28
US-10-038-972A-10
; Sequence 10, Application US/10038972A
; Publication No. US20020192823A1
; GENERAL INFORMATION:
;  APPLICANT: J. Bartlett
;  TITLE OF INVENTION: AAV VECTORS AND METHODS
;  FILE REFERENCE: 28335/36996US
;  CURRENT APPLICATION NUMBER: US/10/038,972A
;  CURRENT FILING DATE:  2002-01-04
;  PRIOR APPLICATION NUMBER: US 60/260,124
;  PRIOR FILING DATE: 2001-01-05
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 4C-RGD Peptide
US-10-038-972A-10

  Query Match             100.0%;  Score 65;  DB 13;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 29
US-10-304-160-3
; Sequence 3, Application US/10304160
; Publication No. US20030099619A1
; GENERAL INFORMATION:
;  APPLICANT: WICKHAM, THOMAS J
;  APPLICANT:  KOVESDI, IMRE
;  APPLICANT:  ROELVINK, PETRUS W
;  APPLICANT:  EINFELD, DAVID
;  APPLICANT:  BROUGH, DOUGLAS E
;  APPLICANT:  LIZONOVA, ALENA
;  TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
;  FILE REFERENCE: 220148
;  CURRENT APPLICATION NUMBER: US/10/304,160
;  CURRENT FILING DATE:  2002-11-25
;  PRIOR APPLICATION NUMBER: PCT/US01/17391
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: US 09/631,191
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 60/208451
;  PRIOR FILING DATE: 2000-05-31
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-304-160-3

  Query Match             100.0%;  Score 65;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 30
US-10-264-374-1
; Sequence 1, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT:  Pasqualini, Renata
;  TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
;  TITLE OF INVENTION:  Molecules That Home to Angiogenic Vasculature Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: P-LJ 3203
;  CURRENT APPLICATION NUMBER: US/10/264,374
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: US/09/139,802
;  PRIOR FILING DATE: 1998-08-25
;  PRIOR APPLICATION NUMBER: 08/926,914
;  PRIOR FILING DATE: 1997-09-10
;  PRIOR APPLICATION NUMBER: 08/710,067
;  PRIOR FILING DATE: 1996-09-10
;  NUMBER OF SEQ ID NOS: 226
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-10-264-374-1

  Query Match             100.0%;  Score 65;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 31
US-10-032-221B-35
; Sequence 35, Application US/10032221B
; Publication No. US20030144481A1
; GENERAL INFORMATION:
;  APPLICANT: Kalluri, Raghuram
;  TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF
;  FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)
;  CURRENT APPLICATION NUMBER: US/10/032,221B
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: PCT/US01/00565
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: US 09/625,191
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 09/543,371
;  PRIOR FILING DATE: 2000-04-04
;  PRIOR APPLICATION NUMBER: US 09/479,118
;  PRIOR FILING DATE: 2000-01-07
;  PRIOR APPLICATION NUMBER: US 09/335,224
;  PRIOR FILING DATE: 1999-06-17
;  PRIOR APPLICATION NUMBER: US 60/126,175
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 60/089,689
;  PRIOR FILING DATE: 1998-06-17
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic blocking peptide
US-10-032-221B-35

  Query Match             100.0%;  Score 65;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 32
US-10-375-992-1
; Sequence 1, Application US/10375992
; Publication No. US20030152578A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruoslahti, Erkki
;                   Pasqualini, Renata
;        TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
;                            Derived Therefrom, and Methods of Using Same
;        NUMBER OF SEQUENCES: 199
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Campbell & Flores
;             STREET: 4370 La Jolla Village Drive, Suite 700
;             CITY: San Diego
;             STATE: California
;             COUNTRY: United States
;             ZIP: 92122
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/375,992
;             FILING DATE: 27-Feb-2003
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/926,914
;             FILING DATE: 10-SEP-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Campbell, Cathryn A.
;             REGISTRATION NUMBER: 31,815
;             REFERENCE/DOCKET NUMBER: P-LJ 2725
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (619) 535-9001
;             TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             TOPOLOGY: both
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-375-992-1

  Query Match             100.0%;  Score 65;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 33
US-10-666-696-450
; Sequence 450, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  APPLICANT:  GUDAS, JEAN MARIE
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527A
;  CURRENT APPLICATION NUMBER: US/10/666,696
;  CURRENT FILING DATE:  2003-09-19
;  PRIOR APPLICATION NUMBER: US/09/563,286C
;  PRIOR FILING DATE: 2000-05-03
;  PRIOR APPLICATION NUMBER: 09/428,082
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1157
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-450
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Query Match 100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 34
US-10-666-696-1076
; Sequence 1076, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-1076

Query Match 100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 35
US-10-653-048-450
; Sequence 450, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-653-048-450

Query Match 100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 36
US-10-653-048-1076
; Sequence 1076, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-653-048-1076

Query Match 100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 37
US-10-264-374-1
; Sequence 1, Application US/10264374
; Publication No. US20040096441A9
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-1

Query Match 100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CDCRGDCFC 9
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Db          1 CDCRGDCFC 9
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Job time : 45 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 11, 2004, 10:00:48 ; Search time 23 Seconds
(without alignments)
20.201 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	9	2	US-08-701-124-3	Sequence 3, Appli
2	65	100.0	9	2	US-08-286-861-16	Sequence 16, Appl
3	65	100.0	9	3	US-09-026-633-1	Sequence 1, Appli
4	65	100.0	9	3	US-09-130-225-3	Sequence 3, Appli
5	65	100.0	9	3	US-09-124-671-33	Sequence 33, Appl
6	65	100.0	9	3	US-09-258-754-211	Sequence 211, App
7	65	100.0	9	3	US-09-139-802-1	Sequence 1, Appli
8	65	100.0	9	3	US-09-042-107-211	Sequence 211, App
9	65	100.0	9	3	US-09-320-424-20	Sequence 20, Appl
10	65	100.0	9	3	US-09-426-680-12	Sequence 12, Appl
11	65	100.0	9	4	US-09-455-061-3	Sequence 3, Appli
12	65	100.0	9	4	US-09-174-943-8	Sequence 8, Appli
13	65	100.0	9	4	US-09-315-127-18	Sequence 18, Appl
14	65	100.0	9	4	US-09-659-786-1	Sequence 1, Appli
15	65	100.0	9	4	US-09-825-563-20	Sequence 20, Appl
16	65	100.0	9	4	US-08-926-914-1	Sequence 1, Appli
17	65	100.0	9	4	US-09-722-250D-211	Sequence 211, App
18	65	100.0	9	4	US-09-969-192-3	Sequence 3, Appli
19	65	100.0	9	4	US-09-428-082B-450	Sequence 450, App
20	65	100.0	9	4	US-09-428-082B-1076	Sequence 1076, Ap
21	65	100.0	9	4	US-09-660-377A-10	Sequence 10, Appl
22	59	90.8	9	2	US-08-286-861-17	Sequence 17, Appl
23	59	90.8	9	4	US-09-428-082B-451	Sequence 451, App
24	56	86.2	8	3	US-09-026-633-4	Sequence 4, Appli
25	51	78.5	9	2	US-08-701-124-4	Sequence 4, Appli
26	51	78.5	9	2	US-08-286-861-15	Sequence 15, Appl
27	51	78.5	9	3	US-09-130-225-4	Sequence 4, Appli
28	51	78.5	9	4	US-09-455-061-4	Sequence 4, Appli
29	51	78.5	9	4	US-09-969-192-4	Sequence 4, Appli
30	51	78.5	9	4	US-09-428-082B-449	Sequence 449, App
31	49	75.4	9	2	US-08-286-861-18	Sequence 18, Appl
32	49	75.4	9	4	US-09-428-082B-452	Sequence 452, App
33	44	67.7	7	3	US-09-426-680-11	Sequence 11, Appl
34	40	61.5	8	1	US-08-421-702A-22	Sequence 22, Appl
35	40	61.5	8	1	US-08-303-052A-22	Sequence 22, Appl
36	40	61.5	8	1	US-08-421-696A-22	Sequence 22, Appl
37	40	61.5	8	1	US-08-421-697A-22	Sequence 22, Appl
38	40	61.5	8	1	US-08-421-698A-22	Sequence 22, Appl
39	40	61.5	8	2	US-08-421-695A-22	Sequence 22, Appl
40	40	61.5	8	5	PCT-US95-04741-22	Sequence 22, Appl
41	38	58.5	7	2	US-08-286-861-14	Sequence 14, Appl
42	35	53.8	5	1	US-08-212-186A-10	Sequence 10, Appl
43	35	53.8	5	1	US-08-425-238-8	Sequence 8, Appli
44	35	53.8	5	2	US-08-625-695A-10	Sequence 10, Appl
45	35	53.8	5	2	US-08-335-832-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-701-124-3
; Sequence 3, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-3

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||||||||
Db 1 CDCRGDCFC 9

RESULT 2
US-08-286-861-16
; Sequence 16, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki

```
;    APPLICANT:  Koivunen, Erkki
;    TITLE OF INVENTION:  No. 5981478el Integrin-Binding Peptides
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,861
;      FILING DATE:  04-AUG-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/158,001
;      FILING DATE:  24-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 9992
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  circular
US-08-286-861-16

  Query Match           100.0%;  Score 65;  DB 2;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 3
US-09-026-633-1
; Sequence 1, Application US/09026633
; Patent No. 6025328
; GENERAL INFORMATION:
;  APPLICANT: McMorris, Trevor C.
;  APPLICANT: Kelner, Michael J.
;  TITLE OF INVENTION: Antitumor agents
;  FILE REFERENCE: 103.008US1
;  CURRENT APPLICATION NUMBER: US/09/026,633
;  CURRENT FILING DATE: 1998-02-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence
US-09-026-633-1

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 4
US-09-130-225-3
; Sequence 3, Application US/09130225
; Patent No. 6057155
;  GENERAL INFORMATION:
;    APPLICANT:  Wickham, Thomas J.
;    APPLICANT:  Roelvink, Petrus W.
;    APPLICANT:  Kovesdi, Imre
;    TITLE OF INVENTION:  TARGETING ADENOVIRUS WITH USE OF
;    TITLE OF INVENTION:  CONSTRAINED PEPTIDE MOTIFS
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza - 49th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/130,225
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 8-701124
;      FILING DATE:  21-AUG-1996
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-130-225-3

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 5
US-09-124-671-33
; Sequence 33, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
;  APPLICANT: Rothman, James
;  APPLICANT: Mayhew, Mark
;  APPLICANT: Hoe, Mee
;  TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
;  FILE REFERENCE: 31488
;  CURRENT APPLICATION NUMBER: US/09/124,671A
;  CURRENT FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: alpha-five integrin binding motif
US-09-124-671-33

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
```

```
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 6
US-09-258-754-211
; Sequence 211, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT: Pasqualini, Renata
;  APPLICANT: Rajotte, Daniel
;  TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
;  TITLE OF INVENTION: Membrane Dipeptidase
;  FILE REFERENCE: P-LJ 3443
;  CURRENT APPLICATION NUMBER: US/09/258,754
;  CURRENT FILING DATE: 1999-02-26
;  EARLIER APPLICATION NUMBER: 09/042,107
;  EARLIER FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 452
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-211

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 7
US-09-139-802-1
; Sequence 1, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT: Pasqualini, Renata
;  TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
;  TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
;  TITLE OF INVENTION: Same
;  FILE REFERENCE: P-LJ 3203
;  CURRENT APPLICATION NUMBER: US/09/139,802
;  CURRENT FILING DATE: 1998-08-25
;  EARLIER APPLICATION NUMBER: 08/926,914
;  EARLIER FILING DATE: 1997-09-10
;  EARLIER APPLICATION NUMBER: 08/710,067
;  EARLIER FILING DATE: 1996-09-10
;  NUMBER OF SEQ ID NOS: 226
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-139-802-1

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 8
US-09-042-107-211
; Sequence 211, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT: Pasqualini, Renata
;  TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
;  TITLE OF INVENTION: Tissues
;  FILE REFERENCE: P-LJ 2892
;  CURRENT APPLICATION NUMBER: US/09/042,107
;  CURRENT FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 436
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-211

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 9
US-09-320-424-20
; Sequence 20, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
;  APPLICANT: Wiley, Steven R.
;  APPLICANT: Goodwin, Raymond G.
;  TITLE OF INVENTION: Cytokine that Induces Apoptosis
;  FILE REFERENCE: 2835-E
;  CURRENT APPLICATION NUMBER: US/09/320,424
;  CURRENT FILING DATE: 1999-05-26
;  EARLIER APPLICATION NUMBER: 09/190,046
;  EARLIER FILING DATE: 1998-11-10
;  EARLIER APPLICATION NUMBER: 09/048,641
;  EARLIER FILING DATE: 1998-03-26
;  EARLIER APPLICATION NUMBER: 08/670,354
;  EARLIER FILING DATE: 1996-06-25
;  EARLIER APPLICATION NUMBER: 08/548,368
;  EARLIER FILING DATE: 1995-11-01
;  EARLIER APPLICATION NUMBER: 08/496,632
;  EARLIER FILING DATE: 1995-06-29
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: artificial
;   OTHER INFORMATION: peptide
US-09-320-424-20

  Query Match           100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
```

```
                  |||||||||
Db          1 CDCRGDCFC 9


RESULT 10
US-09-426-680-12
; Sequence 12, Application US/09426680
; Patent No. 6287857
; GENERAL INFORMATION:
;  APPLICANT: Catherine R. O'Riordan
;  APPLICANT: Samuel C. Wadsworth
;  TITLE OF INVENTION: Nucleic Acid Delivery Vehicles
;  FILE REFERENCE: GA0103USB2
;  CURRENT APPLICATION NUMBER: US/09/426,680
;  CURRENT FILING DATE: 1999-10-25
;  EARLIER APPLICATION NUMBER: PCT/US99/02680
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (0)...(0)
US-09-426-680-12

  Query Match             100.0%;  Score 65;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 11
US-09-455-061-3
; Sequence 3, Application US/09455061
; Patent No. 6329190
;  GENERAL INFORMATION:
;    APPLICANT:  Wickham, Thomas J.
;    APPLICANT:  Roelvink, Petrus W.
;    APPLICANT:  Kovesdi, Imre
;    TITLE OF INVENTION:  TARGETING ADENOVIRUS WITH USE OF
;    TITLE OF INVENTION:  CONSTRAINED PEPTIDE MOTIFS
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza - 49th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/455,061
;      FILING DATE:  06-DEC-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 9-130225
;      FILING DATE:  06-AUG-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 8-701124
;      FILING DATE:  21-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hefner, M. Daniel
;      REGISTRATION NUMBER:  41,826
;      REFERENCE/DOCKET NUMBER:  203128
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-455-061-3

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 12
US-09-174-943-8
; Sequence 8, Application US/09174943
; Patent No. 6420110
; GENERAL INFORMATION:
;  APPLICANT: GYURIS, JENO
;  APPLICANT: MORRIS, AARON J.
;  TITLE OF INVENTION: METHODS AND REAGENTS FOR ISOLATING BIOLOGICALLY ACTIVE
;  TITLE OF INVENTION: PEPTIDES
;  FILE REFERENCE: MIV-106.01
;  CURRENT APPLICATION NUMBER: US/09/174,943
;  CURRENT FILING DATE: 1998-10-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: RGD motif
US-09-174-943-8

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 13
US-09-315-127-18
; Sequence 18, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
;  APPLICANT: The University of Tennessee, c/o Richard Cox
;  TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
;  TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
;  FILE REFERENCE: 44137-5023, U. of Tennessee
;  CURRENT APPLICATION NUMBER: US/09/315,127
;  CURRENT FILING DATE: 1999-05-20
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  SEQ. ID NO.
;   OTHER INFORMATION: 14, alpha Vbeta3-binding peptide
US-09-315-127-18

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 14
US-09-659-786-1
; Sequence 1, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
;  APPLICANT:  Ruoslahti, Erkki
;  APPLICANT:  Pasqualini, Renata
;  TITLE OF INVENTION:  NGR Receptor and Methods of Identifying Tumor Homing
;  TITLE OF INVENTION:  Molecules That Home to Angiogenic Vasculature Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  P-LJ 3203
;  CURRENT APPLICATION NUMBER: US/09/659,786
;  CURRENT FILING DATE:  2000-09-11
;  PRIOR APPLICATION NUMBER:  08/926,914
;  PRIOR FILING DATE:  1997-09-10
;  PRIOR APPLICATION NUMBER:  08/710,067
;  PRIOR FILING DATE:  1996-09-10
;  NUMBER OF SEQ ID NOS:  226
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-659-786-1

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 15
US-09-825-563-20
; Sequence 20, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
;  APPLICANT: Wiley, Steven R.
;  APPLICANT:  Goodwin, Raymond G.
;  TITLE OF INVENTION: Cytokine that Induces Apoptosis
;  FILE REFERENCE: 2835-E
;  CURRENT APPLICATION NUMBER: US/09/825,563
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: 09/320,424
;  PRIOR FILING DATE: 1999-05-26
;  PRIOR APPLICATION NUMBER: 09/190,046
;  PRIOR FILING DATE: 1998-11-10
;  PRIOR APPLICATION NUMBER: 09/048,641
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 08/670,354
;  PRIOR FILING DATE: 1996-06-25
;  PRIOR APPLICATION NUMBER: 08/548,368
;  PRIOR FILING DATE: 1995-11-01
;  PRIOR APPLICATION NUMBER: 08/496,632
;  PRIOR FILING DATE: 1995-06-29
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: artificial
;   OTHER INFORMATION: peptide
US-09-825-563-20

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 16
US-08-926-914-1
; Sequence 1, Application US/08926914
; Patent No. 6576239
;  GENERAL INFORMATION:
;    APPLICANT:  Ruoslahti, Erkki
;    APPLICANT:  Pasqualini, Renata
;    TITLE OF INVENTION:  Tumor Homing Molecules, Conjugates
;    TITLE OF INVENTION:  Derived Therefrom, and Methods of Using Same
;    NUMBER OF SEQUENCES:  199
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/926,914
;      FILING DATE:  10-SEP-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 2725
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  both
;    MOLECULE TYPE:  peptide
US-08-926-914-1

  Query Match             100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 17
US-09-722-250D-211
; Sequence 211, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT:  Pasqualini, Renata
;  TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
;  TITLE OF INVENTION:  Tissues
;  FILE REFERENCE: P-LJ 4514
```

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;  CURRENT APPLICATION NUMBER: US/09/722,250D
;  CURRENT FILING DATE:  2000-11-22
;  PRIOR APPLICATION NUMBER: US 09/042,107
;  PRIOR FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-211

  Query Match            100.0%;  Score 65;  DB 4;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDCRGDCFC 9
              |||||||||
Db          1 CDCRGDCFC 9


RESULT 18
US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. 6649407
;   GENERAL INFORMATION:
;        APPLICANT: WICKHAM, THOMAS J.
;                   ROELVINK, PETRUS W.
;                   KOVESDI, IMRE
;        TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;                            CONSTRAINED PEPTIDE MOTIFS
;        NUMBER OF SEQUENCES: 80
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;             STREET: Two Prudential Plaza - 49th Floor
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/969,192
;             FILING DATE: 01-Oct-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 9-455061
;             FILING DATE: 06-DEC-1999
;             APPLICATION NUMBER: US 9-130225
;             FILING DATE: 06-AUG-1998
;             APPLICATION NUMBER: US 8-701124
;             FILING DATE: 21-AUG-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hefner, M. Daniel
;             REGISTRATION NUMBER: 41,826
;             REFERENCE/DOCKET NUMBER: 213564
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

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  Best Local Similarity  100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CDCRGDCFC 9


RESULT 19
US-09-428-082B-450
; Sequence 450, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-450

  Query Match            100.0%;  Score 65;  DB 4;  Length 9;
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RESULT 20
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; Sequence 1076, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-1076

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RESULT 21
US-09-660-377A-10
; Sequence 10, Application US/09660377A
; Patent No. 6685914
; GENERAL INFORMATION:
;  APPLICANT: Liu, Shuang
;  TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
;  FILE REFERENCE: BMS-2207
;  CURRENT APPLICATION NUMBER: US/09/660,377A
;  CURRENT FILING DATE:  2000-09-12
;  PRIOR APPLICATION NUMBER: 60/153,512
;  PRIOR FILING DATE: 1999-09-13
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Cyclo
US-09-660-377A-10

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Db          1 CDCRGDCFC 9


Search completed: July 11, 2004, 10:06:48
Job time : 23 secs
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